

GenCore version 5.1.5
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 31, 2003, 18:52:35 ; Search time 1352 seconds
(without alignments) 2455.677 Million cell updates/sec

Title: US-09-375-514-22
Perfect score: 1104
Sequence: 1 MAHAGRTGYDNREIVMKYIH.....HTWIQDNGWGWGASGDVSLG 205

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60362

Minimum DB seq length: 10
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlp
-Q=/cgn2.1/USPTO.spool/US09375514/runat_28052003.165345.18673/app_query.fasta.1.391
-DB=EST -QPMF=fastcap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=500
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=10 -MAXLEN=40
-USER=US09375514.@CNG.1.1.1525.@runat_28052003.165345.18673 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST :
1: em_estba : *
2: em_esthum : *
3: em_estin : *
4: em_estma : *
5: em_estov : *
6: em_estpl : *
7: em_estro : *
8: em_hic : *
9: gb_estli : *
10: gb_est2 : *
11: gb_hic : *
12: gb_est3 : *
13: gb_est4 : *
14: gb_est5 : *
15: em_estfun : *
16: em_estom : *
17: gb_gss : *
18: em_gss_hum : *
19: em_gss_inv : *
20: em_gss_pln : *
21: em_gss_vrt : *
22: em_gss_fun : *
23: em_gss_man : *
24: em_gss_mus : *
25: em_gss_other : *
26: em_gss_pro : *
27: em_gss_rod : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	44	4.0	31	9	AA999756	AA999756 os93e04.s
C 2	42	3.8	34	9	AI811024	AI811024 tr03a03.x
C 3	42	3.8	37	9	AI698327	AI698327 tx63c12.x
C 4	41	3.7	34	9	AI202980	AI202980 qr32e08.x
C 5	41	3.7	40	9	AI628006	AI628006 ty21d06.x
C 6	40	3.6	31	9	AI422710	AI422710 tf29d12.x
C 7	40	3.6	36	13	BM010450	BM010450 603631395
C 8	40	3.6	36	13	BM010792	BM010792 603629306
C 9	40	3.6	37	9	AI683252	AI683252 tx02e12.x
C 10	40	3.6	40	2	HSM003700	AI039224 Homo sapi
C 11	39	3.5	27	17	AZ782295	AZ782295 2M0022019
C 12	39	3.5	34	12	BE729288	BE729288 601561653
C 13	38	3.4	31	9	AI912532	AI912532 tz25g07.x
C 14	38	3.4	34	9	AI131930	AI131930 uc33g07.r
C 15	38	3.4	35	17	AZ832681	AZ832681 2M0113H24
C 16	38	3.4	36	10	BE395744	BE395744 601311259
C 17	38	3.4	37	17	AZ580135	AZ580135 1M0368E16
C 18	38	3.4	40	12	BG709439	BG709439 602673496
C 19	37	3.4	29	17	AZ780387	AZ780387 2M0017N12
C 20	37	3.4	33	17	AZ784258	AZ784258 2M0026G22
C 21	37	3.4	34	9	AI217993	AI217993 qf53g10.x
C 22	37	3.4	34	9	AI362411	AI362411 qv92e02.x
C 23	37	3.4	34	9	AI612902	AI612902 ty33d03.x
C 24	37	3.4	37	9	AI761879	AI761879 wg68c11.x
C 25	37	3.4	40	9	AI015468	AI015468 ov54e11.s
C 26	37	3.4	40	9	AI800161	AI800161 tr23b08.x
C 27	36	3.3	24	17	AZ982483	AZ982483 2M0263K16
C 28	36	3.3	27	10	AW250272	AW250272 2821187.5
C 29	36	3.3	31	9	AA871994	AA871994 o105c06.s
C 30	36	3.3	31	9	AA999756	AA999756 os93e04.s
C 31	36	3.3	31	9	AI677781	AI677781 wc80c06.x
C 32	36	3.3	32	13	BI762555	BI762555 603048685
C 33	36	3.3	32	13	BI832949	BI832949 603090781
C 34	36	3.3	32	13	BI833158	BI833158 603090881
C 35	36	3.3	32	13	BI833514	BI833514 603088181
C 36	36	3.3	32	17	AZ320746	AZ320746 1M00040P21
C 37	36	3.3	33	13	BI829654	BI829654 603079396
C 38	36	3.3	34	9	AI589397	AI589397 tr61h11.x
C 39	36	3.3	35	12	BE867678	BE867678 601443224
C 40	36	3.3	35	17	AZ477888	AZ477888 1M0297B02
C 41	36	3.3	36	17	BH792266	BH792266 SALK_0632
C 42	36	3.3	37	9	AA987401	AA987401 oq87g06.s
C 43	36	3.3	37	9	AI357425	AI357425 qu01c09.x
C 44	36	3.3	38	13	BI829338	BI829338 603079491
C 45	36	3.3	40	9	AA869375	AA869375 vq07c10.r
C 46	36	3.3	40	9	AI565182	AI565182 tq56h10.x
C 47	36	3.3	40	17	AZ372178	AZ372178 1M0123J24
C 48	35.5	3.2	38	12	BE867536	BE867536 601443035
C 49	35	3.2	25	9	AI024239	AI024239 ov71g02.s
C 50	35	3.2	30	17	AZ791470	AZ791470 2M0041H21
C 51	35	3.2	30	17	TA211A03P	TA211A03P
C 52	35	3.2	31	9	AI273865	AI273865 qu09a10.x
C 53	35	3.2	31	9	AI287914	AI287914 qul3c06.x
C 54	35	3.2	31	9	AI364457	AI364457 qw38e11.x
C 55	35	3.2	34	9	AA625403	AA625403 af69a08.r
C 56	35	3.2	37	13	BI765481	BI765481 603050546
C 57	35	3.2	38	17	AZ313639	AZ313639 1M0030K04
C 58	35	3.2	39	13	BG973894	BG973894 602843523
C 59	35	3.2	39	14	T17564	T17564 mps v232 Th
C 60	35	3.2	40	9	AA034448	AA034448 zk23a08.s
C 61	35	3.2	40	9	AA878864	AA878864 of84g05.s
C 62	35	3.2	40	9	AI282721	AI282721 qt65c10.x
C 63	34.5	3.1	34	9	AI689593	AI689593 tx84g11.x
C 64	34.5	3.1	34	9	AI915735	AI915735 wg73b11.x

65	34	3.1	25	9	AA878798	of82h02.s	AA878798	of82h02.s	138	33	3.0	40	9	AI288030	qu99e04.x
66	34	3.1	28	9	AI096133	SMOVL3CAN	AI096133	SMOVL3CAN	139	33	3.0	40	9	AI572314	te39f10.x
67	34	3.1	28	17	AZ303959	IM0003P16	AZ303959	IM0003P16	140	33	3.0	40	9	AI630923	tz31h05.x
68	34	3.1	30	17	AZ450779	IM0249K09	AZ450779	IM0249K09	141	33	3.0	40	9	AI758820	ty24h01.x
69	34	3.1	31	9	AA871994	o105c06.s	AA871994	o105c06.s	142	33	3.0	40	9	AI800161	tr23b08.x
70	34	3.1	31	9	AI422710	tf29d12.x	AI422710	tf29d12.x	143	33	3.0	40	9	AA446838	zw84h01.r
71	34	3.1	33	17	AZ380833	IM0136Q21	AZ380833	IM0136Q21	144	33	3.0	40	9	AA568463	nm25d04.s
72	34	3.1	33	17	AZ961620	2M0230F09	AZ961620	2M0230F09	145	33	3.0	40	13	BI753930	603022937
73	34	3.1	33	17	AZ961620	2M0230F09	AZ961620	2M0230F09	146	33	3.0	40	17	BH644925	IM08044A1
74	34	3.1	34	9	AI368216	qy99c06.x	AI368216	qy99c06.x	147	32.5	2.9	40	17	AZ600248	IM0418D11
75	34	3.1	34	9	AZ293547	zt54g12.s	AZ293547	zt54g12.s	148	32.5	2.9	40	17	AZ600248	IM0418D11
76	34	3.1	34	17	AZ591530	IM0401L09	AZ591530	IM0401L09	149	32.5	2.9	40	9	AI653385	ty02b12.x
77	34	3.1	34	17	AZ832181	2M0112K19	AZ832181	2M0112K19	150	32.5	2.9	40	9	AI630583	AL630583
78	34	3.1	34	17	AL759480	ArabiDops	AL759480	ArabiDops	151	32	2.9	40	9	AI088727	qal9e11.x
79	34	3.1	35	17	AZ439115	IM0229N05	AZ439115	IM0229N05	152	32	2.9	40	9	AI088727	qal9e11.x
80	34	3.1	35	17	AZ469734	IM0283J19	AZ469734	IM0283J19	153	32	2.9	40	9	AI088727	qal9e11.x
81	34	3.1	35	17	AZ946037	2M0207G10	AZ946037	2M0207G10	154	32	2.9	40	9	AI088727	qal9e11.x
82	34	3.1	36	9	AL655844	AL655844	AL655844	AL655844	155	32	2.9	40	9	AI088727	qal9e11.x
83	34	3.1	37	9	AA931619	oo35a11.s	AA931619	oo35a11.s	156	32	2.9	40	9	AI088727	qal9e11.x
84	34	3.1	37	9	AL801867	AL801867	AL801867	AL801867	157	32	2.9	40	9	AI088727	qal9e11.x
85	34	3.1	38	17	AZ487251	IM0316A18	AZ487251	IM0316A18	158	32	2.9	40	9	AI088727	qal9e11.x
86	34	3.1	38	17	AZ775686	2M0008H12	AZ775686	2M0008H12	159	32	2.9	40	9	AI088727	qal9e11.x
87	34	3.1	39	17	AZ445435	IM0241B14	AZ445435	IM0241B14	160	32	2.9	40	9	AI088727	qal9e11.x
88	34	3.1	39	17	AZ997025	2M0283J19	AZ997025	2M0283J19	161	32	2.9	40	9	AI088727	qal9e11.x
89	34	3.1	40	9	AI088727	qal9e11.x	AI088727	qal9e11.x	162	32	2.9	40	9	AI088727	qal9e11.x
90	34	3.1	40	14	D21036	HUMGS02019	D21036	HUMGS02019	163	32	2.9	40	9	AI088727	qal9e11.x
91	34	3.1	40	17	AZ320260	IM0040A15	AZ320260	IM0040A15	164	32	2.9	40	9	AI088727	qal9e11.x
92	33.5	3.0	37	12	BF036425	601460458	BF036425	601460458	165	32	2.9	40	9	AI088727	qal9e11.x
93	33.5	3.0	37	9	AZ275360	vc07404.r	AZ275360	vc07404.r	166	32	2.9	40	9	AI088727	qal9e11.x
94	33	3.0	39	17	AZ344511	IM0031B20	AZ344511	IM0031B20	167	32	2.9	40	9	AI088727	qal9e11.x
95	33	3.0	39	17	AZ324865	IM0047G10	AZ324865	IM0047G10	168	32	2.9	40	9	AI088727	qal9e11.x
96	33	3.0	40	23	AZ861432	2M0167E24	AZ861432	2M0167E24	169	32	2.9	40	9	AI088727	qal9e11.x
97	33	3.0	40	25	AZ861588	IM0168J04	AZ861588	IM0168J04	170	32	2.9	40	9	AI088727	qal9e11.x
98	33	3.0	40	26	AZ588958	IM0397B09	AZ588958	IM0397B09	171	32	2.9	40	9	AI088727	qal9e11.x
99	33	3.0	40	28	AZ623372	ts18e04.x	AZ623372	ts18e04.x	172	32	2.9	40	9	AI088727	qal9e11.x
100	33	3.0	40	28	AZ687937	tp99a01.x	AZ687937	tp99a01.x	173	32	2.9	40	9	AI088727	qal9e11.x
101	33	3.0	40	30	AZ375563	IM0128P24	AZ375563	IM0128P24	174	32	2.9	40	9	AI088727	qal9e11.x
102	33	3.0	40	30	AZ864869	2M0174M09	AZ864869	2M0174M09	175	32	2.9	40	9	AI088727	qal9e11.x
103	33	3.0	40	30	AZ995340	2M0281E11	AZ995340	2M0281E11	176	32	2.9	40	9	AI088727	qal9e11.x
104	33	3.0	40	31	AZ689315	tx93f07.x	AZ689315	tx93f07.x	177	32	2.9	40	9	AI088727	qal9e11.x
105	33	3.0	40	31	AZ485617	IM0313G08	AZ485617	IM0313G08	178	32	2.9	40	9	AI088727	qal9e11.x
106	33	3.0	40	31	DM1225	Danio rer	DM1225	Danio rer	179	32	2.9	40	9	AI088727	qal9e11.x
107	33	3.0	40	31	BM398978	5009-0-51	BM398978	5009-0-51	180	32	2.9	40	9	AI088727	qal9e11.x
108	33	3.0	40	33	AZ627977	IM0476L03	AZ627977	IM0476L03	181	32	2.9	40	9	AI088727	qal9e11.x
109	33	3.0	40	34	AI128655	q862f02.s	AI128655	q862f02.s	182	32	2.9	40	9	AI088727	qal9e11.x
110	33	3.0	40	34	AI217993	qf52g10.x	AI217993	qf52g10.x	183	32	2.9	40	9	AI088727	qal9e11.x
111	33	3.0	40	34	AI278110	qm63b12.x	AI278110	qm63b12.x	184	32	2.9	40	9	AI088727	qal9e11.x
112	33	3.0	40	34	AI396645	fb15d12.x	AI396645	fb15d12.x	185	32	2.9	40	9	AI088727	qal9e11.x
113	33	3.0	40	34	AI539355	te51a08.x	AI539355	te51a08.x	186	32	2.9	40	9	AI088727	qal9e11.x
114	33	3.0	40	34	AZ635438	IM0491J15	AZ635438	IM0491J15	187	32	2.9	40	9	AI088727	qal9e11.x
115	33	3.0	40	34	BH811595	SALK_0591	BH811595	SALK_0591	188	32	2.9	40	9	AI088727	qal9e11.x
116	33	3.0	40	34	BH811595	SALK_0591	BH811595	SALK_0591	189	32	2.9	40	9	AI088727	qal9e11.x
117	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	190	32	2.9	40	9	AI088727	qal9e11.x
118	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	191	32	2.9	40	9	AI088727	qal9e11.x
119	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	192	32	2.9	40	9	AI088727	qal9e11.x
120	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	193	32	2.9	40	9	AI088727	qal9e11.x
121	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	194	32	2.9	40	9	AI088727	qal9e11.x
122	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	195	32	2.9	40	9	AI088727	qal9e11.x
123	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	196	32	2.9	40	9	AI088727	qal9e11.x
124	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	197	32	2.9	40	9	AI088727	qal9e11.x
125	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	198	32	2.9	40	9	AI088727	qal9e11.x
126	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	199	32	2.9	40	9	AI088727	qal9e11.x
127	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	200	32	2.9	40	9	AI088727	qal9e11.x
128	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	201	32	2.9	40	9	AI088727	qal9e11.x
129	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	202	32	2.9	40	9	AI088727	qal9e11.x
130	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	203	32	2.9	40	9	AI088727	qal9e11.x
131	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	204	32	2.9	40	9	AI088727	qal9e11.x
132	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	205	32	2.9	40	9	AI088727	qal9e11.x
133	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	206	32	2.9	40	9	AI088727	qal9e11.x
134	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	207	32	2.9	40	9	AI088727	qal9e11.x
135	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	208	32	2.9	40	9	AI088727	qal9e11.x
136	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	209	32	2.9	40	9	AI088727	qal9e11.x
137	33	3.0	40	35	BH811595	SALK_0591	BH811595	SALK_0591	210	32	2.9	40	9	AI088727	qal9e11.x

211	32	2.9	38	10	AV960043	AV960043	284	31	2.8	34	9	AI354356
c 212	32	2.9	38	13	BG912318	602806861	c 285	31	2.8	34	9	AI370143
c 213	32	2.9	38	17	AZ344442	1M0078P20	286	31	2.8	34	9	AA282064
c 214	32	2.9	38	17	AZ390541	1M0151021	287	31	2.8	34	13	BM398554
c 215	32	2.9	38	17	AZ402445	1M0169D13	288	31	2.8	34	14	N30949
c 216	32	2.9	38	17	AZ490125	1M0322J19	289	31	2.8	34	17	AZ309860
c 217	32	2.9	38	17	AZ588936	1M0397M05	290	31	2.8	34	17	AZ377095
c 218	32	2.9	38	17	AZ657455	1M0533H08	c 291	31	2.8	35	9	AU260290
c 219	32	2.9	38	17	AZ765843	1M0563B04	c 292	31	2.8	35	13	BM398666
c 220	32	2.9	38	17	AZ863994	2M0173B22	c 293	31	2.8	35	17	AZ317100
c 221	32	2.9	39	9	AL775941	AL775941	c 294	31	2.8	35	17	AZ440999
c 222	32	2.9	39	12	BF344480	602014879	c 295	31	2.8	35	17	AZ843372
c 223	32	2.9	39	17	AQ025109	EP(3)0545	c 296	31	2.8	35	17	AZ848745
c 224	32	2.9	39	17	AZ588176	1M0396M11	c 297	31	2.8	36	10	BE296967
c 225	32	2.9	39	17	AZ657728	1M0534B08	c 298	31	2.8	36	10	BE298656
c 226	32	2.9	39	17	DR11A19T	AL734670	299	31	2.8	36	13	BI861680
c 227	32	2.9	40	9	AA872575	Danlo rer	300	31	2.8	37	9	AA701135
c 228	32	2.9	40	9	AI089757	qa216h08.s	c 301	31	2.8	37	9	AI048978
c 229	32	2.9	40	9	AI569502	cn87h04.x	c 302	31	2.8	37	9	AI475333
c 230	32	2.9	40	9	AI609582	tw28c02.x	c 303	31	2.8	37	9	AI538439
c 231	32	2.9	40	9	AI741783	gr22h02.x	c 304	31	2.8	37	9	AI625989
c 232	32	2.9	40	9	AI745660	wt24e02.x	c 305	31	2.8	37	9	AA186584
c 233	32	2.9	40	10	BE296536	601174028	c 306	31	2.8	37	9	AL652018
c 234	32	2.9	40	13	BJ035979	BU035979	c 307	31	2.8	37	10	AV966952
c 235	32	2.9	40	13	BM398163	BM398163	c 308	31	2.8	37	10	AW248135
c 236	32	2.9	40	17	AZ628038	1M0476N17	c 309	31	2.8	37	13	BM396191
c 237	32	2.9	40	17	AZ776089	2M0009A03	c 310	31	2.8	37	17	AZ514419
c 238	31.5	2.9	40	17	BH800882	1M08028B1	c 311	31	2.8	37	17	AZ817852
c 239	31.5	2.9	28	9	AI287864	qv07d12.x	c 312	31	2.8	37	17	AZ819838
c 240	31.5	2.9	31	9	AI375455	tc25c09.x	c 313	31	2.8	37	17	TA211Bi1P
c 241	31.5	2.9	35	17	AZ666583	IM0548N17	c 314	31	2.8	38	9	AL787489
c 242	31.5	2.9	40	9	AI619702	ty52a05.x	c 315	31	2.8	38	10	AV949462
c 243	31.5	2.9	40	9	AA878861	of84f09.s	c 316	31	2.8	38	13	BI835970
c 244	31	2.8	19	17	AZ445563	1M0241P18	c 317	31	2.8	38	13	BI835970
c 245	31	2.8	20	17	AZ609449	1M0434D20	c 318	31	2.8	38	17	AB081861
c 246	31	2.8	22	9	AI679776	cu76f02.x	c 319	31	2.8	38	17	TA222A09P
c 247	31	2.8	22	17	AZ862318	2M0169N13	c 320	31	2.8	39	9	AI1811713
c 248	31	2.8	23	17	AZ442547	AZ442547	c 321	31	2.8	39	10	AV953675
c 249	31	2.8	24	17	AZ346754	1M0082BE12	c 322	31	2.8	39	10	AV959991
c 250	31	2.8	24	17	AZ403170	1M0170A19	c 323	31	2.8	39	12	BG112163
c 251	31	2.8	25	9	AI138565	qd85a07.x	c 324	31	2.8	39	12	BG112163
c 252	31	2.8	25	9	AI632809	tz32e04.x	c 325	31	2.8	39	13	BM398130
c 253	31	2.8	26	17	AZ361612	as86h10.x	c 326	31	2.8	39	13	BM398130
c 254	31	2.8	27	14	B0540272	PTAM0589	c 327	31	2.8	39	17	BH791816
c 255	31	2.8	27	14	B0540272	PTAM0589	c 328	31	2.8	40	9	AA878864
c 256	31	2.8	27	14	B0540272	PTAM0589	c 329	31	2.8	40	9	AA878864
c 257	31	2.8	27	17	AZ809574	2M0074C18	c 330	31	2.8	40	9	AA931142
c 258	31	2.8	28	9	AI174332	ai17d02.s	c 331	31	2.8	40	9	AA931142
c 259	31	2.8	28	9	AI416657	sal0b04.x	c 332	31	2.8	40	9	AA939192
c 260	31	2.8	28	17	AZ371137	IM0122C01	c 333	31	2.8	40	9	AA123696
c 261	31	2.8	29	14	T56973	ya83h12.r1	c 334	31	2.8	40	9	AA123696
c 262	31	2.8	29	17	AZ774255	2M0003L24	c 335	31	2.8	40	9	AA123696
c 263	31	2.8	30	17	TA179D12P	AL74655 T. brucei	c 336	31	2.8	40	9	AA123696
c 264	31	2.8	31	9	AA883594	al46d08.s	c 337	31	2.8	40	12	BF343276
c 265	31	2.8	31	9	AI003715	Z903c07.s	c 338	31	2.8	40	12	BF343276
c 266	31	2.8	31	9	AI242643	qu37e10.x	c 339	31	2.8	40	13	BM397619
c 267	31	2.8	31	9	AI445875	tj12h07.x	c 340	31	2.8	40	13	BM398139
c 268	31	2.8	31	9	AI559535	tq50c01.x	c 341	31	2.8	40	13	BM399151
c 269	31	2.8	31	9	AI708294	as31c03.x	c 342	31	2.8	40	14	R22729
c 270	31	2.8	31	9	AI793967	fc56504.x	c 343	31	2.8	40	14	R22729
c 271	31	2.8	31	17	AZ343319	IM0078G16	c 344	31	2.8	40	17	CNS07EUR
c 272	31	2.8	31	17	AZ424646	1M0204B20	c 345	30.5	2.8	40	17	TA149A04P
c 273	31	2.8	31	17	AZ796042	2M0051B13	c 346	30.5	2.8	40	17	AZ840388
c 274	31	2.8	31	17	AZ969178	2M0241A19	c 347	30.5	2.8	40	17	AI619558
c 275	31	2.8	32	13	B1192552	602945447	c 348	30.5	2.8	40	17	AZ805273
c 276	31	2.8	32	13	B1545769	603187918	c 349	30.5	2.8	40	17	AZ805273
c 277	31	2.8	32	17	AZ815018	2M0083G02	c 350	30.5	2.8	40	17	AZ805273
c 278	31	2.8	33	9	AU255884	AU255884	c 351	30.5	2.8	40	17	AZ805273
c 279	31	2.8	33	13	BI330146	602983757	c 352	30.5	2.8	40	17	AZ805273
c 280	31	2.8	33	13	BI914099	603182037	c 353	30	2.7	40	9	AI039253
c 281	31	2.8	33	17	AZ972050	2M0245G14	c 354	30	2.7	40	9	AI039253
c 282	31	2.8	33	17	BH810319	SALK_0491	c 355	30	2.7	40	9	AI039253
c 283	31	2.8	34	9	AI035422	ub46d08.r	c 356	30	2.7	40	9	AI039253

C 357 2.7 25 9 AA873288 9A873288 Oh68h09.s C 430 30 2.7 37 9 AA902929
C 358 30 2.7 25 9 AI298122 AI298122 qm64e06.x C 431 30 2.7 37 9 AI124999 ai124999 ok43f02.s
C 359 30 2.7 25 9 AI664044 AI664044 ue47e05.r C 432 30 2.7 37 9 AI129902 qc41b07.x
C 360 30 2.7 25 17 AZ603284 AZ603284 1M0422E01 C 433 30 2.7 37 9 AI287459 ai287459 q99d07.x
C 361 30 2.7 25 17 AZ632343 AZ632343 1M0486K22 C 434 30 2.7 37 9 AI357088 ai357088 qx16d03.x
C 362 30 2.7 25 17 AZ872633 AZ872633 2M0186K01 C 435 30 2.7 37 9 AI49210 ai49210 to08e02.x
C 363 30 2.7 25 17 BH812755 BH812755 SALK_0630 C 436 30 2.7 37 9 AI582521 ai582521 ts02a03.x
C 364 30 2.7 25 17 BH856288 BH856288 SALK_0810 C 437 30 2.7 37 9 AI689454 ai689454 tx94c06.x
C 365 30 2.7 26 17 AZ786827 AZ786827 2M0032N07 C 438 30 2.7 37 9 AI699754 ai699754 tz12b01.x
C 366 30 2.7 26 17 BH814118 BH814118 SALK_0657 C 439 30 2.7 37 9 AI755616 ai755616 EtEStea38
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C 368 30 2.7 27 17 AZ768008 AZ768008 1M0567D14 C 441 30 2.7 37 9 AL677081 AL677081 AL677081
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C 372 30 2.7 28 9 AI416657 AI416657 sal0b04.x C 445 30 2.7 37 17 AZ836826 AZ836826 2M0131A20
C 373 30 2.7 28 9 AI916689 AI916689 tu89f07.x C 446 30 2.7 37 17 TA354G01Q TA354G01Q T. brucei
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C 392 30 2.7 33 17 AZ57580 AZ57580 1M0367M15 C 465 30 2.7 37 17 AZ836826 AZ836826 2M0131A20
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C 421 30 2.7 36 13 BI819025 BI819025 60303150 C 494 30 2.7 37 17 AZ836826 AZ836826 2M0131A20
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C 428 30 2.7 37 9 AA778469 AA778469 af20d01.s C 500 30 2.7 37 17 AZ836826 AZ836826 2M0131A20

ALIGNMENTS

RESULT 1
AA999756/c 31 bp mRNA linear EST 05-JUN-1998
LOCUS OS93e04.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1612926 3'
DEFINITION similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;, mRNA sequence.
ACCESSION AA999756
VERSION AA999756.1 GI:3190311
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 31)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb@remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1612926"
/clone_lib="NCI_CGAP_GC3"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

3 a 11 c 16 g 1 t

ALIGNMENT Scores:

Pred. No.: 1.09e+05 Length: 31
Score: 44.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 3.99% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AA999756 (1-31)

QY 39 ProProGlyAlaAlaProAlaProGly 47
||||||| :|||
Db 30 CGCGCCGACCTCTCTCTCGCCCGGG 4

RESULT 2

AA1811024 34 bp mRNA linear EST 07-JUL-1999
LOCUS tr03a03.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2217196 3'
DEFINITION similar to TR:P92327 P92327 PROLINE-RICH PROTEIN PRP2 PRECURSOR.
; contains element MSK1 repetitive element ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AA1811024
AA1811024.1 GI:5397590
EST.
human.
Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 34)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb@remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2217196"
/clone_lib="NCI_CGAP_Ov23"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"
BASE COUNT 10 a 17 c 6 g 1 t

ALIGNMENT Scores:

Pred. No.: 1.77e+05 Length: 34
Score: 42.00 Matches: 7
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 3.80% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AA1811024 (1-34)

QY 39 ProProGlyAlaAlaProAlaProGly 47
||||||| |||||
Db 4 CCCCCGAAAGCCCCCCCCCGGGA 30

RESULT 3

AA1698327/c

LOCUS tx63c12.x1 NCI_CGAP_Utl1 Homo sapiens cDNA clone IMAGE:2274262 3'
DEFINITION similar to TR:Q41120 Q41120 HYDROXYPROLINE-RICH GLYCOPROTEIN ;, mRNA sequence.
ACCESSION AA1698327
VERSION AA1698327.1 GI:4986227
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1039 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source

1. 37
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2274262"
/clone_lib="NCI-CGAP_Utl"
/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site.1: SalI;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"

BASE COUNT 9 a 7 c 21 g 0 t
ORIGIN

Alignment Scores:
Pred. No.: 1.94e+05 Length: 37
Score: 42.00 Matches: 7
Percent Similarity: 72.73% Conservative: 1
Best Local Similarity: 63.64% Mismatches: 3
Query Match: 3.80% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AI698327 (1-37)

Qy 39 ProProGlyAlaAlaProAlaProGlyIlePhe 49
|||||
Db 37 CCCCCGGGGCCCCCCCCCTCCCGCTGTTT 5

RESULT 4
AI202980

LOCUS AI202980 34 bp mRNA linear EST 14-OCT-1998
DEFINITION qr32e08.x1 NCI-CGAP_GC6 Homo sapiens CDNA clone IMAGE:1942598 3'
similar to TR:Q08805 Q08805 SALIVARY PROLINE-RICH PROTEIN L
:contains element MSRI repetitive element ;, mRNA sequence.

ACCESSION AI202980
VERSION AI202980.1 GI:3755586
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 34)

REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Unpublished (1997)

JOURNAL COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

FEATURES
source

1. 34
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1942598"
/clone_lib="NCI-CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pW7T3D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; Plasmid DNA
from the normalized library NCI-CGAP_GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258631, 1459064-1470983, and 1475592-1476743).
1257096-1258631, 1459064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 3 a 22 c 9 g 0 t
ORIGIN

Alignment Scores:
Pred. No.: 2.14e+05 Length: 34
Score: 41.00 Matches: 7
Percent Similarity: 63.64% Conservative: 0
Best Local Similarity: 63.64% Mismatches: 4
Query Match: 3.71% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AI202980 (1-34)

Qy 36 GlyAlaAlaProGlyAlaAlaProAlaPro 46
|||
Db 1 GGGGGCCCCCCCCAGGCAAGCCCCCCCCCCC 33

RESULT 5
AI628006/c

LOCUS AI628006 40 bp mRNA linear EST 07-MAR-2000
DEFINITION ty21d06.x1 NCI-CGAP_Ut3 Homo sapiens CDNA clone IMAGE:2279723 3'
similar to TR:Q43687 Q43687 EXTENSIN-LIKE PROTEIN ;contains element
MSRI repetitive element ;, mRNA sequence.

ACCESSION AI628006
VERSION AI628006.1 GI:4664806
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 40)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

JOURNAL COMMENT
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1838 Std Error: 0.00
Seq primer: -40UP from Gibco

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers

High quality sequence stop: 1
POLYA=No.

FEATURES

source

Location/Qualifiers
1. 40
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:229723"
/clone_lib="NCI_CGAP_Ut3"
/tissue_type="poorly-differentiated endometrial
adenocarcinoma, 2 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018"

BASE COUNT 8 a 11 c 18 g 3 t
ORIGIN

Alignment Scores:

Red. No.: 2.56e+05 Length: 40
Score: 41.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 3.71% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AF628006 (1-40)

QY 41 GlyAlaAlaProAlaProGlyIlePheSerSerGlnPro 53

DB 40 GGGGGCCCCAGACCCGGGTGTTCCTCTCCCT 2

RESULT 6

AI422710/c

LOCUS

DEFINITION AI422710 31 bp mRNA linear EST 30-MAR-1999
tf29d12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2097623 3'
similar to SW:CAL3_BOVIN P04258 COLLAGEN ALPHA 1(III) CHAIN.
; contains element MSRI repetitive element ;, mRNA sequence.

ACCESSION AI422710.1 GI:4268641

VERSION AI422710

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/RTGAP), Tumor Gene Index

Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 616 Std Error: 0.00
Seq primer: -40bp from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. 31

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2097623"

/clone_lib="NCI_CGAP_Brn23"

FEATURES

source

/tissue_type="glioblastoma (pooled)"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAGTGGGAGCGGCATATCTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT 3 a 12 c 15 g 1 t
ORIGIN

Alignment Scores:

Red. No.: 2.33e+05 Length: 31
Score: 40.00 Matches: 7
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 3.62% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AI422710 (1-31)

QY 39 ProProGlyAlaAlaProAlaProGly 47

DB 30 CCCCCGGGGCCCCCTTGGCCGGG 4

RESULT 7

BM010450/c

LOCUS

DEFINITION BM010450 36 bp mRNA linear EST 30-OCT-2001
603631395F1 NTH_MGC_41 Homo sapiens cDNA clone IMAGE:5445310 5',
mRNA sequence.

ACCESSION BM010450

VERSION BM010450.1 GI:16524804

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DPF

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LICM1925 row: m column: 23

High quality sequence stop: 36.

Location/Qualifiers

1. 36

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5445310"

/clone_lib="NIH_MGC_41"

/tissue_type="amelanotic melanoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:

EcoRI; cDNA made by oligo-dr priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

BASE COUNT 7 a 11 c 16 g 2 t
ORIGIN

36 ATGGGGGGGTCCCCCTCAGGGCCCTGGCTCCTCCTCCC 1

RESULT 9	AI683252	linear	EST 16-DEC-1999
LOCUS	AI683252	37 bp	mrna
DEFINITION	tx02el2.x1 NCI_CCAP_ut4 Homo sapiens cDNA clone IMAGE:2268046 3' similar to TR:Q04118 Q04118 SALIVARY PROLINE-RICH GLYCOPROTEIN G1 PRECURSOR. ; contains TAR1.b2 MSR1 repetitive element;; mRNA		

sequence.
ACCESSION AI683252
VERSION AI683252.1 GI:4893434
KEYWORDS EST.
SOURCE human.

REFERENCE
1 (bases 1 to 37)
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

AUTHORS
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
NCI-CCGAP Project (CCGAP)

**JOURNAL
COMMENT**

tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be

Alignment Scores:	2.76e+05	Length:	36
Pred. No.:	40.00	Matches:	7
Score:	40.00	Conservative:	2
Percent Similarity:	75.00%	Mismatches:	3
Best Local Similarity:	58.33%	Indels:	0
Query Match:	3.62%	Caps:	0
Gap:	13		

US-09-375-514-22 (1-205) x BM010450 (1-36)

QY 35 ValcylAlaAlaProGlyAlaAlaProAlaPro 46
:::|||||:::|||||
:::|||||:::|||||

RESULT 8	BM010792	36 bp	mRNA	linear	EST 30-OCT-2001
BM010792/c					
LOCUS					

mRNA sequence.

ACCESSION BM010792

VERSION BM010792.1

KEYWORDS EST.

GI:16535146

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo
1 (bases 1 to 36)
REFERENCE NH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM506 row: j column: 14.
Location/Qualifiers

FEATURES

source

1. .34
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:383127"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT

8 a 5 c 15 g 6 t

ORIGIN

Alignment Scores:
Pred. No.: 3.13e+05 Length: 34
Score: 39.00 Matches: 6
Percent Similarity: 88.89% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 3.53% Indels: 0
DB: 12 Gaps: 0

US-09-375-514-22 (1-205) x BE729288 (1-34)

QY

38 AlapProGlyAlaAlaProAlaPro 46

Db

34 TCACCACCGGGCTCGACCTAGCCCT 8

RESULT 13

AI912532/c

LOCUS

AI912532 31 bp mRNA linear EST 16-DEC-1999
t225q07.x1 NCI-CGAP.Ut2 Homo sapiens cDNA clone IMAGE:2289660 3'
similar to TR:056971 056971 ORF FOR OVERLAPPING PROTEIN. ; contains
MER22.b2 MSRI repetitive element ;, mRNA sequence.

ACCESSION

AI912532

VERSION

AI912532.1 GI:5632387

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 31)

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 1799 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers
1. .31
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2289660"
/clone_lib="NCI-CGAP.Ut2"
/tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"

BASE COUNT

6 a 22 c 0 g 3 t

ORIGIN

Alignment Scores:
Pred. No.: 3.4e+05 Length: 31
Score: 38.00 Matches: 5
Percent Similarity: 85.71% Conservative: 1
Best Local Similarity: 71.43% Mismatches: 1
Query Match: 3.44% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AI912532 (1-31)

QY

191 AspAsnGlyGlyTrpValGly 197

Db

30 GATGGGGGGGGTGGATTGGG 10

RESULT 14

AI131930

LOCUS

AI131930

DEFINITION

uc33907.x1 Soares_mammary_gland_NbMWG Mus musculus cDNA clone
IMAGE:1399836 5' similar to TR:035034 035034 CPE-RECEPTOR. ;, mRNA
sequence.

ACCESSION

AI131930

VERSION

AI131930.1 GI:3601946

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 34)

AUTHORS

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE

The WashU-HMI Mouse EST Project

JOURNAL

Unpublished (1996)

COMMENT

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:911552

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1. .34

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:1399836"
 /clone_lib="Soares_mammary_gland_NbMMG"
 /sex="male"
 /tissue_type="mammary gland"
 /dev_stage="4 weeks"
 /lab_host="DH10B"

/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 3 a 13 c 10 g 8 t
 ORIGIN

Alignment Scores:
 Pred. No.: 3 76e+05 Length: 34
 Score: 38.00 Matches: 7
 Percent Similarity: 88.89% Conservative: 1
 Best Local Similarity: 77.78% Mismatches: 1
 Query Match: 3.44% Indels: 0
 DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x A1131930 (1-34)

QY 43 AlaProAlaProGlyIlePheSerSer 51

DB 4 GCTCCAGCTCCGTGGCTACTGTCTAGC 30

RESULT 15

AZ832681

LOCUS 2M0113H24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0113H24 F, DNA sequence.

ACCESSION AZ832681

VERSION AZ832681.1 GI:13002685

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 35)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Plasmid inserts

Mouse whole genome scaffolding with paired end reads from 10kb

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0113 row: H column: 24

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 35.

Location/Qualifiers

1..35

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0113H24"

FEATURES
 source

/clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 2 c 20 g 7 t
 ORIGIN

Alignment Scores:
 Pred. No.: 3 89e+05 Length: 35
 Score: 38.00 Matches: 6
 Percent Similarity: 77.78% Conservative: 1
 Best Local Similarity: 66.67% Mismatches: 2
 Query Match: 3.44% Indels: 0
 DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x AZ832681 (1-35)

QY 192 AsnGlyGlyTrpValGlyAlaSerGly 200

DB 4 AATCGCGGTGGATGGAGTGGTGGG 30

RESULT 16

BE395744

LOCUS 601311259F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632655 5',

DEFINITION mRNA sequence.

ACCESSION BE395744

VERSION BE395744.1 GI:93411109

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 36)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC

CNA Library Preparation: Ling Hong/Rubin Laboratory

CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLC324 row: f column: 16

High quality sequence stop: 36.

Location/Qualifiers

1..36

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3632655"

/clone_lib="NIH_MGC_44"

/tissue_type="endometrium, adenocarcinoma cell line"

FEATURES
 source

constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT
ORIGIN

5 a 15 c 15 g 5 t

Alignment Scores:

Pred. No.: 4.51e+05 Length: 40
Score: 38.00 Matches: 8
Percent Similarity: 72.73% Conservative: 0
Best Local Similarity: 72.73% Mismatches: 3
Query Match: 3.44% Indels: 0
DB: 12 Gaps: 0

US-09-375-514-22 (1-205) x BG709439 (1-40)

QY 75 ProAlaAlaProGlyAlaAlaGlyProAla 85

DB 33 CGAAGGCGACGGCTGCAGCGGGGACCCGCT 1

RESULT 19

AZ780387

LOCUS

DEFINITION 29 bp DNA linear GSS 16-FEB-2001
clone UUGC2M0017N12 R, DNA sequence.

ACCESSION

VERSION AZ780387.1 GI:12911997

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 29)
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0017 row: N column: 12

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

1..29

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0017N12"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

1 a 0 c 23 g 5 t

Alignment Scores:

Pred. No.: 3.81e+05 Length: 29
Score: 37.00 Matches: 6
Percent Similarity: 85.71% Conservative: 0
Best Local Similarity: 85.71% Mismatches: 1
Query Match: 3.35% Indels: 0
DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x AZ780387 (1-29)

QY 194 GlyTTPValGlyAlaSerGly 200

DB 3 GGGTGGTGGGGGGGAGTGGG 23

RESULT 20

AZ784258/c

LOCUS

DEFINITION 33 bp DNA linear GSS 16-FEB-2001
clone UUGC2M0026G22 R, DNA sequence.

ACCESSION

VERSION AZ784258

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 33)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0026 row: G column: 22

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 33.

Location/Qualifiers

1..33

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0026G22"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (91473211419b1AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 7 c 16 g 8 t

ORIGIN

Alignment Scores:

Pred. No.: 4.4e+05 Length: 33
Score: 37.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 3.35% Indels: 0
DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x AZ784258 (1-33)

Qy 54 GlyHisThrProHisPro 59

Db 25 GGGCACTGGCCGCCACCC 8

RESULT 21

LOCUS

DEFINITION

q52910.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753698
3' similar to SW:CALL_MOUSE P11087 PROCOLLAGEN ALPHA 1(I) CHAIN
PRECURSOR. ; contains MER22.b3 MSRI MSRI repetitive element ; , mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 826 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. 34

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1753698"

/clone_lib="Soares_testis_NHT"

/sex="male"

/lab_host="DH10B"

/note="vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from Clontech Laboratories

, Inc., and primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGGCGGCCCAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 2 a 11 c 18 g 3 t

ORIGIN

Alignment Scores:

Pred. No.: 4.55e+05 Length: 34
Score: 37.00 Matches: 6
Percent Similarity: 66.67% Conservatives: 0
Best Local Similarity: 66.67% Mismatches: 3
Query Match: 3.35% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AI217993 (1-34)

Qy 39 ProProGlyAlaAlaProAlaProGly 47

Db 31 CGCGCGGGCGCCGCCGCCGCGCTGGT 5

RESULT 22

LOCUS

DEFINITION

AI362411 34 bp mRNA linear EST 06-JAN-1999
qV92602.x1 NCI-CGAP_Ut2 Homo sapiens cDNA clone IMAGE:1989050 3'
similar to SW:CALL_RAT P02454 COLLAGEN ALPHA 1(I) CHAIN ; contains
element MER22 repetitive element ; , mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers

1. 34

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1989050"

/clone_lib="NCI-CGAP_Ut2"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="DH10B"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.85 kb. Life Technologies catalog #:

11539-012"

BASE COUNT 0 a 15 c 18 g 1 t

ORIGIN

Alignment Scores:

Pred. No.: 4.55e+05 Length: 34
Score: 37.00 Matches: 6

ACCESSION AI015468
 VERSION AI015468.1 GI:3229804
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 40)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 JOURNAL Tumor Gene Index
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
 , Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Trace considered overall poor quality
 Insert Length: 500 Std Error: 0.00
 Seq primer: -40m13 fwd. Et from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..40
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1641164"
 /clone_lib="Soares_testis_NHT"
 /sex="male"
 /lab_host="DH10B"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from Clontech Laboratories
 , Inc., and primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGGAGCGCCGCCCAATTTTTTTTTTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT7T3 vector. Library
 went through one round of normalization to Cot5, and was
 constructed by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 4 a 13 c 16 g 7 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 5,45e+05 Length: 40
 Score: 37.00 Matches: 7
 Percent Similarity: 58.33% Conservativeness: 0
 Best Local Similarity: 58.33% Mismatches: 5
 Query Match: 3.35% Indels: 0
 DB: 9 Gaps: 0
 US-09-375-514-22 (1-205) x AI015468 (1-40)
 Qy 35 ValGlyAlaProGlyAlaProGlyAlaProAlaPro 46
 Db 1 GTGGCGCGTTCGCCGACGCTCCAGGACCTTGCGC 36
 RESULT 26
 AI800161 40 bp mRNA linear EST 06-JUL-1999
 LOCUS tr23b08.x1 NCI-CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219127 3'
 DEFINITION similar to SW:CAL3_BOVIN P04258 COLLAGEN ALPHA 1(III) CHAIN.
 ; contains element MSRI repetitive element ;, mRNA sequence.
 ACCESSION AI800161 GI:5365633
 VERSION AI800161.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 40)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 JOURNAL Tumor Gene Index
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
 , Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Trace considered overall poor quality
 Insert Length: 500 Std Error: 0.00
 Seq primer: -40m13 fwd. Et from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..40
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1641164"
 /clone_lib="Soares_testis_NHT"
 /sex="male"
 /lab_host="DH10B"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from Clontech Laboratories
 , Inc., and primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGGAGCGCCGCCCAATTTTTTTTTTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT7T3 vector. Library
 went through one round of normalization to Cot5, and was
 constructed by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 4 a 13 c 16 g 7 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 5,45e+05 Length: 40
 Score: 37.00 Matches: 7
 Percent Similarity: 58.33% Conservativeness: 0
 Best Local Similarity: 58.33% Mismatches: 5
 Query Match: 3.35% Indels: 0
 DB: 9 Gaps: 0
 US-09-375-514-22 (1-205) x AI015468 (1-40)
 Qy 35 ValGlyAlaProGlyAlaProGlyAlaProAlaPro 46
 Db 1 GTGGCGCGTTCGCCGACGCTCCAGGACCTTGCGC 36
 RESULT 26
 AI800161 40 bp mRNA linear EST 06-JUL-1999
 LOCUS tr23b08.x1 NCI-CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219127 3'
 DEFINITION similar to SW:CAL3_BOVIN P04258 COLLAGEN ALPHA 1(III) CHAIN.
 ; contains element MSRI repetitive element ;, mRNA sequence.
 ACCESSION AI800161 GI:5365633
 VERSION AI800161.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 40)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 JOURNAL Tumor Gene Index
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
 , Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Trace considered overall poor quality
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers
 1..40
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2219127"
 /clone_lib="NCI-CGAP_Ov23"
 /tissue_type="tumor, 5 pooled (see description)"
 /lab_host="DH10B"
 /note="Organ: ovary; Vector: pCMV-SPORT6; Site.1: SalI;
 Site.2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.35 kb. Tumor types include: mixed
 Mullerian tumor, papillary serous, clear cell, spindle
 cell. All are primary tumors, metastasis positive. Life
 Technologies catalog #: 11534-013"
 TECHNOLOGIES catalog #: 11534-013
 BASE COUNT 1 a 23 c 14 g 1 t 1 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 5,45e+05 Length: 40
 Score: 37.00 Matches: 7
 Percent Similarity: 66.67% Conservativeness: 1
 Best Local Similarity: 58.33% Mismatches: 4
 Query Match: 3.35% Indels: 0
 DB: 9 Gaps: 0
 US-09-375-514-22 (1-205) x AI800161 (1-40)
 QY 54 GlyHisThrProHisProAlaAlaSerArgAspPro 65
 Db 1 GGGCCCTCCCGCCCCCGGGCGCCCGGGGACCG 36
 RESULT 27
 AZ982483 24 bp DNA linear GSS 27-APR-2001
 LOCUS 2M0263K16F Mouse 10kb plasmid UUCG2M library Mus musculus genomic
 DEFINITION clone UUCG2M0263K16 F, DNA sequence.
 ACCESSION AZ982483 GI:13853710
 VERSION AZ982483.1
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center

University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0263 row: K column: 16
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES

Location/Qualifiers
 1. 24
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0263K16"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 2 a 1 c 17 g 4 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.73e+05 Length: 24
 Score: 36.00 Matches: 6
 Percent Similarity: 85.71% Conservative: 0
 Best Local Similarity: 85.71% Mismatches: 1
 Query Match: 3.26% Indels: 0
 DB: 17 Gaps: 0
 US-09-375-514-22 (1-205) x AZ982483 (1-24)
 QY 194 GlyTnpValGlyAlaSerGly 200
 Db 1 GGGTGGGTAGGGAGCTGTGG 21
 RESULT 28
 AW250272/c
 LOCUS
 DEFINITION
 AW250272 27 bp mRNA linear EST 07-JAN-2000
 2821187.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821187 5',
 mRNA sequence.
 AW250272
 VERSION
 AW250272.1 GI:6593265
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 27)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Other_ESTs: 2821187.3prime

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
 project clone distribution: MGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
 Scores: PHRED from University of Washington Genome Center. Vector
 Trimming: cross match from University of Washington Genome Center. Vector
 PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
 Drosophila Genome Project. University of Washington Genome Center:
 http://www.genome.washington.edu Low Quality Sequence: 9 contiguous
 PHRED high quality bases following vector sequence. Very Low
 Quality Sequence: Trace file contained 27 contiguous distinct peaks
 following vector sequence.
 Plate: LUCM6 row: C column: 12
 High quality sequence stop: 9.

FEATURES

Location/Qualifiers
 1. 27
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2821187"
 /clone_lib="NIH_MGC_7"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life technologies)."

BASE COUNT 2 a 7 c 15 g 3 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 4.25e+05 Length: 27
 Score: 36.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 3.26% Indels: 0
 DB: 10 Gaps: 0
 US-09-375-514-22 (1-205) x AW250272 (1-27)
 QY 54 GlyHisThrProHisProAlaAla 61
 Db 24 GGCGGCACACGCGACCTCGTGCC 1

RESULT 29
 AA871994/c
 LOCUS
 DEFINITION
 AA871994 31 bp mRNA linear EST 14-APR-1998
 oi05c06.s1 NCI_CGAP_G4 Homo sapiens cDNA clone IMAGE:1475626 3',
 similar to WP:T22D1.2 CE17246 ;, mRNA sequence.
 AA871994
 VERSION
 AA871994.1 GI:2968032
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 31)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 Emmert-Buck, M.D., Ph.D.

/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

BASE COUNT 3 a 16 c 10 g 2 t
ORIGIN

Alignment Scores:

Pred. No.: 4.96e+05 Length: 31
Score: 36.00 Matches: 6
Percent Similarity: 66.67% Conservative: 0
Best Local Similarity: 66.67% Mismatches: 3
Query Match: 3.26% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x At677781 (1-31)

QY 34 AspValGlyAlaAlaProGlyAla 42

Db 27 GACGCGGGGGTGTCCCGCGGGCGG 1
|||||

RESULT 32

BI762555/c

LOCUS BI762555 32 bp mRNA linear EST 25-SEP-2001
DEFINITION 603048685F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188724 5',
mRNA sequence.

ACCESSION BI762555

VERSION BI762555.1 GI:15754133

KEYWORDS EST.

SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM11471 row: j column: 21

High quality sequence stop: 32.

Location/Qualifiers

FEATURES

source

1..32
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5188724"
/lab_host="DH10B"

/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

BASE COUNT 12 a 4 c 15 g 1 t

ORIGIN

Alignment Scores:

Pred. No.: 5.14e+05 Length: 32
Score: 36.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1

Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.26% Indels: 0
DB: 13 Gaps: 0

US-09-375-514-22 (1-205) x BI762555 (1-32)

QY 84 ProAlaLeuSerProValPro 91

Db 30 CCGCCTGTGTCCGCTGCCTCCA 7
|||||

RESULT 33

BI832949/c

LOCUS BI832949

DEFINITION 603090781F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5229596 5',
mRNA sequence.

ACCESSION BI832949

VERSION BI832949.1 GI:15944499

KEYWORDS EST.

SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM11578 row: a column: 21

High quality sequence stop: 32.

Location/Qualifiers

FEATURES

source

1..32
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5229596"
/lab_host="DH10B"

/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA

source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

BASE COUNT 12 a 4 c 15 g 1 t

ORIGIN

Alignment Scores:

Pred. No.: 5.14e+05 Length: 32
Score: 36.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.26% Indels: 0
DB: 13 Gaps: 0

US-09-375-514-22 (1-205) x BI832949 (1-32)

QY 84 ProAlaLeuSerProValPro 91

Db 30 CCGCCTGTGTCTCCGCTGCCTCCA 7
|||||

RESULT 34

BI833158/c

LOCUS BI833158

32 bp mRNA linear EST 04-OCT-2001

DEFINITION 60309081F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5229597 5',
mRNA sequence.
ACCESSION BI833158
VERSION BI833158.1 GI:15944708
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 32)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLMI1578 row: a column: 22
High quality sequence stop: 32.
Location/Qualifiers
1. 32
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5229597"
/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
male. Library is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT 12 a 4 c 15 g 1 t
ORIGIN
Alignment Scores:
Pred. No.: 5.14e+05 Length: 32
Score: 36.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.26% Indels: 0
DB: 13 Gaps: 0
US-09-375-514-22 (1-205) x BI833158 (1-32)
QY 84 ProAlaLeuSerProValPro 91
Db 30 CCGCTCTCTCTCCGCTGCTCCA 7
RESULT 35
BI833514/c 5.14e+05 Length: 32
LOCUS BI833514.1 GI:15945064 32 bp mRNA linear EST 04-OCT-2001
DEFINITION 603088181F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5226933 5',
mRNA sequence.
ACCESSION BI833514
VERSION BI833514.1 GI:15945064
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 32)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLMI1578 row: a column: 22
High quality sequence stop: 32.
Location/Qualifiers
1. 32
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5229597"
/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
male. Library is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT 12 a 4 c 15 g 1 t
ORIGIN
Alignment Scores:
Pred. No.: 5.14e+05 Length: 32
Score: 36.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.26% Indels: 0
DB: 13 Gaps: 0
US-09-375-514-22 (1-205) x BI833158 (1-32)
QY 84 ProAlaLeuSerProValPro 91
Db 30 CCGCTCTCTCTCCGCTGCTCCA 7
RESULT 35
BI833514/c 5.14e+05 Length: 32
LOCUS BI833514.1 GI:15945064 32 bp mRNA linear EST 04-OCT-2001
DEFINITION 603088181F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5226933 5',
mRNA sequence.
ACCESSION BI833514
VERSION BI833514.1 GI:15945064
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 32)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLMI1578 row: a column: 22
High quality sequence stop: 32.
Location/Qualifiers
1. 32
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5229597"
/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
male. Library is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT 12 a 4 c 15 g 1 t
ORIGIN
Alignment Scores:
Pred. No.: 5.14e+05 Length: 32
Score: 36.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.26% Indels: 0
DB: 13 Gaps: 0
US-09-375-514-22 (1-205) x BI833514 (1-32)
QY 84 ProAlaLeuSerProValPro 91
Db 30 CCGCTCTCTCTCCGCTGCTCCA 7
RESULT 36
AZ320746/c 5.14e+05 Length: 32 bp DNA linear GSS 29-SEP-2000
LOCUS AZ320746.1 GI:10372836 32 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0040P21R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0040P21 R, DNA sequence.
ACCESSION AZ320746
VERSION AZ320746.1 GI:10372836
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 32)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLMI1571 row: b column: 22
High quality sequence stop: 32.
Location/Qualifiers
1. 32
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5226933"
/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
male. Library is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT 12 a 4 c 15 g 1 t
ORIGIN
Alignment Scores:
Pred. No.: 5.14e+05 Length: 32
Score: 36.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.26% Indels: 0
DB: 13 Gaps: 0
US-09-375-514-22 (1-205) x BI833514 (1-32)
QY 84 ProAlaLeuSerProValPro 91
Db 30 CCGCTCTCTCTCCGCTGCTCCA 7
RESULT 36
AZ320746/c 5.14e+05 Length: 32 bp DNA linear GSS 29-SEP-2000
LOCUS AZ320746.1 GI:10372836 32 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0040P21R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0040P21 R, DNA sequence.
ACCESSION AZ320746
VERSION AZ320746.1 GI:10372836
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 32)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0040 row: P column: 21
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 32.
 Location/Qualifiers

FEATURES

1..32 source
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG1M0040p21"
 /clone_lib="Mouse 10kb plasmid UUCG1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114[gblAF129072.1]), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 7 c 12 g 7 t
 ORIGIN

Alignment Scores:
 Pred. No.: 5.14e+05 Length: 32
 Score: 36.00 Matches: 6
 Percent Similarity: 60.00% Conservative: 0
 Best Local Similarity: 60.00% Mismatches: 4
 Query Match: 3.26% Indels: 0
 DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x AZ320746 (1-32)

QY 54 GlyHisThrProHisProAlaSerArg 63
 ||| ||||| ||||| |||||
 Db 31 GGGCAACTCCCTCATCCACAGGATCGGA 2

RESULT 37

BI829654/c
 LOCUS
 DEFINITION 603079396f1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5171207 5', mRNA sequence.

ACCESSION BI829654.1 GI:15941204
 VERSION BI829654
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
 Plate: LLAM1425 row: P column: 24
 High quality sequence stop: 33.
 Location/Qualifiers

FEATURES

1..33 source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5171207"
 /clone_lib="NIH_MGC_119"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site: 1; NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

BASE COUNT 12 a 4 c 16 g 1 t
 ORIGIN

Alignment Scores:
 Pred. No.: 5.32e+05 Length: 33
 Score: 36.00 Matches: 6
 Percent Similarity: 87.50% Conservative: 1
 Best Local Similarity: 75.00% Mismatches: 1
 Query Match: 3.26% Indels: 0
 DB: 13 Gaps: 0

US-09-375-514-22 (1-205) x BI829654 (1-33)

QY 84 ProAlaLeuSerProValPro 91
 ||| ||||| ||||| |||||

Db 31 CCGCCTCTGTCCTCCGCTGCTCCA 8

RESULT 38

LOCUS AI589397

DEFINITION

AI589397 34 bp mRNA linear EST 21-APR-1999
 tr61h11.x2 NCI_CGAP_Panl Homo sapiens cDNA clone IMAGE:2222853 3', similar to TR:Q04154 Q04154 SALIVARY PROLINE-RICH PROTEIN RPL15 PRECURSOR. ; contains element MSRL repetitive element ; , mRNA sequence.

ACCESSION AI589397
 VERSION AI589397.1 GI:4598445

KEYWORDS

SOURCE

ORGANISM

human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov

Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES

SOURCE

1..34
 Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2222853"

/clone_lib="NCI_CGAP_Panl"

/tissue_type="adenocarcinoma"
 /lab_host="DH10B"
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.72 kb. Life Technologies catalog #:
 11548-013"

BASE COUNT 4 a 18 c 12 g 0 t

ORIGIN

Alignment Scores:
 Pred. No.: 5.5e+05 Length: 34
 Score: 36.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 3.26% Indels: 0
 DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AT589397 (1-34)

QY 40 ProGlyAlaAlaProAlaProgly 47
 DB 11 CCGGGGGCCACCGCCGCCCGGG 34

RESULT 39

BE867678

LOCUS

DEFINITION 601443224F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847541 5',
 mRNA sequence.

ACCESSION

BE867678

VERSION

BE867678.1 GI:10316454

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 35)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM9561 row: P column: 06

High quality sequence stop: 35.

Location/Qualifiers

1..35

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3847541"

/clone_lib="NIH_MGC_65"

/tissue_type="adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.8 kb. Library constructed by Life
 Technologies."

7 a 15 c 5 g 8 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 5.68e+05 Length: 35

Score: 36.00 Matches: 6

Percent Similarity: 70.00% Conservative: 1

Best Local Similarity: 60.00% Mismatches: 3

Query Match: 3.26% Indels: 0

DB: 12 Gaps: 0

US-09-375-514-22 (1-205) x BE867678 (1-35)

QY 175 LeuTrpMetThrGluTyrLeuAsnArgHis 184
 DB 2 CTTGGATGACATTCATTCGTCAGCTCCAC 31

RESULT 40

AZ477888/c

LOCUS

DEFINITION 1M0297B02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0297B02 R, DNA sequence.

ACCESSION AZ477888

VERSION AZ477888.1

KEYWORDS GI:10636074

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0297 row: B column: 02

Seq primer: CACACAGGAAACACCTATGACC

Class: plasmid ends

High quality sequence stop: 35.

Location/Qualifiers

1..35

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0297B02"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi4732114|gbAF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

2 a 4 c 17 g 12 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 5.68e+05 Length: 35

Score: 36.00 Matches: 5

Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 83.33% Mismatches: 0
 Query Match: 3.26% Indels: 0
 DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x A477888 (1-35)

QY 55 HisThrProHisProAla 60
 Db 34 CACACCCCCACCCAGC 17
 |||||||

RESULT 41

BH792266 36 bp DNA linear GSS 02-APR-2002
 LOCUS SALK_063236.51.15.x Arabidopsis thaliana TDNA insertion lines
 DEFINITION Arabidopsis thaliana genomic clone SALK_063236.51.15.x, DNA
 sequence.

ACCESSION BH792266
 VERSION BH792266.1 GI:19888854
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 36)

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
 ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
 , Zimmermann,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome

JOURNAL Unpublished (2001)

COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated intron of At5g52330.
 Class: TDNA tagged.

FEATURES Location/Qualifiers
 source 1..36

/organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"

/clone="SALK_063236.51.15.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 13 a 4 c 8 g 11 t

Alignment Scores:

Pred. No.: 5.86e+05 Length: 36
 Score: 36.00 Matches: 5
 Percent Similarity: 87.50% Conservative: 2
 Best Local Similarity: 62.50% Mismatches: 1
 Query Match: 3.26% Indels: 0
 DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x BH792266 (1-36)

QY 185 LeuHisThrTrpIleGlnAspAsn 192

Db 5 CTAGAGACATGGTTGGAAGACAAT 28
 ||| |||||||

RESULT 42

AA987401/c
 LOCUS

DEFINITION Oq87906.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1593370 3',
 similar to TR:Q99322 Q99322 MOCIN CORE POLYPEPTIDE, TRACHEAL
 ; contains element LI repetitive element ;, mRNA sequence.

ACCESSION AA987401
 VERSION AA987401.1 GI:3172765

KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 37)

REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
 Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Stratagene, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.

FEATURES Location/Qualifiers
 source 1..37

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1593370"

/clone_lib="NCI_CGAP_Kid6"
 /sex="mixed"

/tissue_type="kidney tumor"
 /lab_host="SOLR (kanamycin resistant)"

/note="Organ: Kidney; Vector: Bluescript SK-; Site_1:
 EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. Pooled kidney tumors. 5' adaptor sequence: 5'
 GAATTCGACGAG 3' 3' adaptor sequence: 5'
 CTCGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."

BASE COUNT 4 a 1 c 19 g 13 t

Alignment Scores:

Pred. No.: 6.04e+05 Length: 37
 Score: 36.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 83.33% Mismatches: 0
 Query Match: 3.26% Indels: 0
 DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AA987401 (1-37)

QY 55 HisThrProHisProAla 60

Db 30 CACACACACACCCATCA 13
 |||||||

RESULT 43

AI357425 37 bp mRNA linear EST 15-FEB-1999
 LOCUS qu01c09.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:1963504 3',
 similar to SW:EXTN_DAUCA P06599 EXTENSIN PRECURSOR, ; contains
 MSRI.b3 MSRI repetitive element ;, mRNA sequence.

ACCESSION AI357425

VERSION AI357425.1 GI:4109046

KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 37)

AUTHORS

NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL

Tumor Gene Index

COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

Clone Sequencing by: Washington University Genome Sequencing Center

CDNA distribution: NCI-CCGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 1215 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..37

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1963504"

/clone_lib="NCI-CCGAP_Col4"

/tissue_type="moderately-differentiated adenocarcinoma"

/lab_host="DH10B"

/note="Organ: Colon; Vector: pCMV-SPORT6; Site:1: SalI;

Site:2: NotI; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 1.7 kb. Life Technologies catalog #:

11531-019"

5 a 25 c 7 g 0 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 5 6.04e+05 Length: 37

Score: 36.00 Matches: 7

Percent Similarity: 63.64% Conservative: 0

Best Local Similarity: 63.64% Mismatches: 4

Query Match: 3.26% Indels: 0

DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AI357425 (1-37)

Qy 53 ProGlyH1sThrProH1sProAlaAlaSerArg 63

||||| ||||| ||||| ||||| |||||

5 CCGGAGCACCACCCCGCCCGCCGCGCACCCG 37

RESULT 44

BI829358/c

LOCUS

DEFINITION

603079491F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5170966 5',

mRNA sequence.

ACCESION

BI829358

VERSION

BI829358.1 GI:15940908

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 38)

NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Trace considered overall poor quality

Insert Length: 1215 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..38

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5170966"

/clone_lib="NIH_MGC_119"

/tissue_type="medulla"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NotI;

Site:2: EcoRV (destroyed); RNA source normal medulla from

anonymous male age 27. Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.3 kb, insert size range

0.9-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 013. Note:

this is a NIH_MGC Library."

12 a 7 c 17 g 2 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 12 6.22e+05 Length: 38

Score: 36.00 Matches: 6

Percent Similarity: 87.50% Conservative: 1

Best Local Similarity: 75.00% Mismatches: 1

Query Match: 3.26% Indels: 0

DB: 13 Gaps: 0

US-09-375-514-22 (1-205) x BI829358 (1-38)

Qy 84 ProAlaLeuSerProValProPro 91

||||| ||||| ||||| ||||| |||||

36 CCGCTCTGTCCTCGCTGCTGCCCTCCA 13

RESULT 45

AA869375/c

LOCUS

DEFINITION

AA869375 40 bp mRNA linear EST 16-MAR-1998

Vq07c10.r1 Barstead stromal cell line MPLRB8 Mus musculus CDNA

clone IMAGE:1093554 5' similar to FR:Q14883 Q14883 INTESINAL MUCIN

;; mRNA sequence.

ACCESION

AA869375

VERSION

AA869375.1 GI:2964820

KEYWORDS

EST.

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 40)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:599786

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28ml3 rev2 ET from Amersham

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

High quality sequence stop: 38.

Location/Qualifiers

1..38

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5170966"

/clone_lib="NIH_MGC_119"

/tissue_type="medulla"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NotI;

Site:2: EcoRV (destroyed); RNA source normal medulla from

anonymous male age 27. Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.3 kb, insert size range

0.9-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 013. Note:

this is a NIH_MGC Library."

12 a 7 c 17 g 2 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 12 6.22e+05 Length: 38

Score: 36.00 Matches: 6

Percent Similarity: 87.50% Conservative: 1

Best Local Similarity: 75.00% Mismatches: 1

Query Match: 3.26% Indels: 0

DB: 13 Gaps: 0

US-09-375-514-22 (1-205) x BI829358 (1-38)

Qy 84 ProAlaLeuSerProValProPro 91

||||| ||||| ||||| ||||| |||||

36 CCGCTCTGTCCTCGCTGCTGCCCTCCA 13

RESULT 45

AA869375/c

LOCUS

DEFINITION

AA869375 40 bp mRNA linear EST 16-MAR-1998

Vq07c10.r1 Barstead stromal cell line MPLRB8 Mus musculus CDNA

clone IMAGE:1093554 5' similar to FR:Q14883 Q14883 INTESINAL MUCIN

;; mRNA sequence.

ACCESION

AA869375

VERSION

AA869375.1 GI:2964820

KEYWORDS

EST.

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 40)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:599786

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 1.

FEATURES
source

1. 40
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1093554"
/clone_lib="Barstead stromal cell line MPLRB8"
/cell_line="C2C12 (undifferentiated)"
/lab_host="DH10B"
/note="Vector: pMT3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Source undifferentiated tissue culture cell line C2C12. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins."

BASE COUNT 1 a 4 c 23 g 12 t

ORIGIN

Alignment Scores:

Pred. No.: 6.58e+05 Length: 40
Score: 36.00 Matches: 5
Percent Similarity: 85.71% Conservative: 1
Best Local Similarity: 71.43% Mismatches: 1
Query Match: 3.26% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AA869375 (1-40)

QY 53 ProGlyHisThrProHisPro 59

Db 40 CCCACCACCTCACCGCCCA 20

RESULT 46

AI565182/c

LOCUS

DEFINITION t956h10.x1 NCI_CGAP_Utl Homo sapiens cDNA clone IMAGE:2212867 3' similar to TR:Q01943 Q01943 EXTENSION ; contains element TARI repetitive element ;, mRNA sequence.

ACCESSION AI565182

VERSION AI565182.1 GI:4523639

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 40)

REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

TITLE Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 2429 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA-No.

FEATURES Location/Qualifiers

source

1. 40
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2212867"
/clone_lib="NCI_CGAP_Utl"
/tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

BASE COUNT 15 a 6 c 19 g 0 t

ORIGIN

Alignment Scores:
Pred. No.: 6.58e+05 Length: 40
Score: 36.00 Matches: 7
Percent Similarity: 66.67% Conservative: 1
Best Local Similarity: 58.33% Mismatches: 4
Query Match: 3.26% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AI565182 (1-40)

QY 46 ProGlyIlePheSerSerGlnProGlyHisThrPro 57

Db 37 CCTTTTCTTTTCTTCCCTCCCGGGGGTCCCCC 2

RESULT 47

AZ372178/c

LOCUS

DEFINITION AZ372178 40 bp DNA linear GSS 02-OCT-2000
1M0123724R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0123J24 R, DNA sequence.

ACCESSION AZ372178

VERSION AZ372178.1 GI:10485878

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 40)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0123 row: J column: 24

Seq primer: CACACGAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 40.

Location/Qualifiers

1. 40

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0123J24"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

musculus C57BL/6J (male) was obtained from the Jackson

musculus C57BL/6J (male) was obtained from the Jackson

musculus C57BL/6J (male) was obtained from the Jackson

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI-. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 9 a 6 c 15 g 10 t
ORIGIN

Alignment Scores: 40
Pred. No.: 6.58e+05 Length: 7
Score: 36.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 3.26% Indels: 0
DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x AZ372178 (1-40)

QY 86 LeuSerProValProProValHisLeuAlaLeuArg 98
|||||
Db 40 CTCAAACCTGCCACAGCTCTCGGAATCTCTACTAGG 2

RESULT 48

BE867536/c 38 bp mRNA linear EST 20-OCT-2000
LOCUS BE867536
DEFINITION 601443035F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847280 5',
mRNA sequence.

ACCESSION BE867536
VERSION BE867536.1 GI:10316312
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 38)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM9561 row: e column: 09

High quality sequence stop: 38.

FEATURES

source

1..38
Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3847280"

/clone_lib="NIH_MGC_65"

/tissue_type="adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 1.8 kb. Library constructed by Life Technologies."

BASE COUNT 4 a 16 c 16 g 2 t
ORIGIN

Alignment Scores: 38
Pred. No.: 6.83e+05 Length: 38
Score: 35.50 Matches: 8
Percent Similarity: 76.92% Conservative: 2
Best Local Similarity: 61.54% Mismatches: 2
Query Match: 3.22% Indels: 1
DB: 12 Gaps: 1

US-09-375-514-22 (1-205) x BE867536 (1-38)

QY 36 GlyAlaAlaProGlyAlaAlaProAlaProGlyIle 48
|||||
Db 36 GGCTCTCG---CGGGCGCGCGCGCGCGCGAGGTA 1

RESULT 49

AI024239 25 bp mRNA linear EST 18-JUN-1998

LOCUS AI024239
DEFINITION ov71g02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1642802
3' similar to TR:002402 002402 INSOLUBLE PROTEIN. ;, mRNA sequence.

ACCESSION AI024239

VERSION AI024239.1 GI:3239283

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 25)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo

, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40ml3 fwd. EF from Amersham

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

source

1..25
Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1642802"

/clone_lib="Soares_testis_NHT"

/sex="male"

/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from Clontech Laboratories

, Inc., and primed with a Not I - oligo(dT) primer [5'

TGTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization to Cot5, and was

constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 10 a 14 c 0 g 1 t

ORIGIN

Alignment Scores:

Pred. No.: 4.72e+05 Length: 25

Score: 35.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.17% Indels: 0
DB: 9 Gaps: 0
US-09-375-514-22 (1-205) x A1024239 (1-25)
QY 55 HisThProHisPro 59
DB 3 CACACACACACCCA 17

RESULT 50
AZ791470/c
LOCUS
DEFINITION
2M0041H21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0041H21 F, DNA sequence.

ACCESSION AZ791470
VERSION AZ791470.1 GI:12934389
KEYWORDS GSS.
SOURCE house mouse.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 30)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.

Mus whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0041 row: H column: 21
Seq primer: CGTTGTAAACGACGCGCCAGT

Class: plasmid ends
High quality sequence stop: 30.

Location/Qualifiers
1..30
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0041H21"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

5 a 1 c 17 g 7 t

BASE COUNT
ORIGIN

Alignment Scores:
Pred. No.: 5.78e+05
Score: 35.00
Percent Similarity: 75.00%
Best Local Similarity: 75.00%
Query Match: 3.17%
DB: 17
US-09-375-514-22 (1-205) x AZ791470 (1-30)

QY 84 ProAlaLeuSerProValProPro 91
DB 28 CCACCTCTCTCAGCCCACTCCACCC 5

Search completed: May 31, 2003, 23:22:20
Job time : 1377 secs

GenCore version 5.1.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 31, 2003, 22:26:00 ; Search time 126 Seconds
(without alignments)
2193.769 Million cell updates/sec

Title: US-09-375-514-22
Perfect score: 1104
Sequence: 1 MAHAGRTGVDNREIVMKYIH.....HTWIQDNGWVGASGDVSLG 205

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 471460

Minimum DB seq length: 10
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool/US09375514/runat_28052003_165346_18724/app_query.fasta_1.391
-DB=Published Applications_NA -QFWT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS-human40.cdi -LISP=500 -DOCLIGN=200 -THR SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=50 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500
-MINLEN=10 -MAXLEN=40
-USER=US09375514.@Cgn_1_1_98@runat_28052003_165346_18724 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	44	4.0	24	9	US-09-970-820-11
C 2	44	4.0	24	9	US-09-986-718-11
C 3	44	4.0	24	10	US-09-371-900-11
C 1	44	4.0	24	9	US-09-970-820-11
C 2	44	4.0	24	9	US-09-986-718-11
C 3	44	4.0	24	10	US-09-371-900-11

33	3.8	42	C 4	9	US-09-963-761B-18	Sequence 18, Appl
31	3.7	41	C 5	10	US-09-925-67A-3	Sequence 3, Appl1
31	3.5	39	C 6	10	US-09-801-274-465	Sequence 465, App
31	3.5	38.5	C 7	10	US-09-801-274-465	Sequence 372, App
22	3.4	38	C 8	9	US-09-931-732-21	Sequence 21, Appl
30	3.4	38	C 9	9	US-09-984-842-2	Sequence 2, Appl1
31	3.4	38	C 10	10	US-09-801-274-943	Sequence 943, App
38	3.4	38	C 11	9	US-10-125-635A-370	Sequence 370, App
38	3.4	38	C 12	9	US-09-938-864-370	Sequence 370, App
38	3.4	38	C 13	9	US-09-785-019-370	Sequence 370, App
38	3.4	38	C 14	9	US-10-002-603-370	Sequence 370, App
37	3.4	37	C 15	10	US-09-920-342-11	Sequence 11, Appl
25	3.4	37	C 16	9	US-10-060-756A-2700	Sequence 2701, Ap
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33	3.4	37	C 18	9	US-09-801-274-1740	Sequence 34, Appl
33	3.4	37	C 19	9	US-09-874-503-34	Sequence 34, Appl
33	3.4	37	C 20	9	US-10-000-157-34	Sequence 34, Appl
33	3.4	37	C 21	9	US-09-747-259-34	Sequence 34, Appl
33	3.4	37	C 22	9	US-09-908-827-34	Sequence 34, Appl
40	3.4	37	C 23	10	US-09-245-802-71	Sequence 71, Appl
37	3.4	37	C 24	10	US-09-734-846-34	Sequence 34, Appl
36	3.3	36	C 25	10	US-09-734-847A-45	Sequence 45, Appl
36	3.3	36	C 26	9	US-09-911-904-37	Sequence 37, Appl
25	3.3	36	C 27	10	US-09-866-108-4774	Sequence 4774, Ap
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25	3.3	36	C 33	10	US-09-866-108-4780	Sequence 4780, Ap
25	3.3	36	C 34	10	US-09-866-108-4781	Sequence 4781, Ap
28	3.3	36	C 35	10	US-09-817-387-11	Sequence 11, Appl
29	3.3	36	C 36	10	US-09-949-145-28	Sequence 28, Appl
30	3.3	36	C 37	9	US-10-245-206-8	Sequence 8, Appl1
30	3.3	36	C 38	10	US-09-291-129-8	Sequence 8, Appl1
32	3.3	36	C 39	10	US-09-801-274-1215	Sequence 1215, Ap
32	3.3	36	C 40	9	US-09-854-356-15	Sequence 15, Appl
35	3.3	36	C 41	9	US-10-000-512-23	Sequence 23, Appl
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27	3.2	35.5	C 44	10	US-09-735-363A-2	Sequence 2, Appl1
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25	3.2	35	C 49	10	US-09-866-108-4468	Sequence 4468, Ap
25	3.2	35	C 50	10	US-09-866-108-4469	Sequence 4469, Ap
25	3.2	35	C 51	10	US-09-866-108-4470	Sequence 4470, Ap
25	3.2	35	C 52	10	US-09-866-108-4471	Sequence 4471, Ap
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33	3.2	35	C 61	10	US-09-925-674A-1	Sequence 1, Appl1
35	3.2	35	C 62	10	US-09-791-502-5	Sequence 5, Appl1
37	3.2	35	C 63	9	US-09-913-238-5	Sequence 5, Appl1
37	3.2	35	C 64	9	US-09-877-478-4006	Sequence 4006, Ap
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20	3.1	34	C 70	10	US-09-832-648-7	Sequence 7, Appl1
20	3.1	34	C 71	10	US-09-832-648-23	Sequence 23, Appl
20	3.1	34	C 72	10	US-09-827-998-936	Sequence 936, App
25	3.1	34	C 73	10	US-09-827-998-937	Sequence 937, App
25	3.1	34	C 74	8	US-08-591-486B-116	Sequence 116, App
28	3.1	34	C 75	30	US-09-953-052-51	Sequence 51, Appl
30	3.1	34	C 76	9	US-10-175-268-6	Sequence 6, Appl1

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79	34	3.1	30	10	US-09-803-549-6	Sequence 6, Appli	c 152	34	3.1	39	9	US-10-080-980-24	Sequence 24, Appli
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88	34	3.1	36	10	US-09-932-129-4	Sequence 4, Appli	c 161	33	3.0	21	9	US-09-959-519-7	Sequence 7, Appli
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91	34	3.1	37	9	US-09-989-735-463	Sequence 463, App	c 164	33	3.0	25	9	US-10-215-112-4515	Sequence 4515, Ap
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93	34	3.1	37	9	US-09-989-730-463	Sequence 463, App	c 166	33	3.0	25	9	US-10-215-112-4339	Sequence 4639, Ap
94	34	3.1	37	9	US-09-990-436-463	Sequence 463, App	c 167	33	3.0	25	9	US-10-215-112-4784	Sequence 4784, Ap
95	34	3.1	37	9	US-09-991-181-463	Sequence 463, App	c 168	33	3.0	25	9	US-10-215-112-8311	Sequence 8311, Ap
96	34	3.1	37	9	US-09-993-687-463	Sequence 463, App	c 169	33	3.0	25	9	US-10-215-112-8437	Sequence 8437, Ap
97	34	3.1	37	9	US-09-989-734-463	Sequence 463, App	c 170	33	3.0	25	9	US-10-215-112-11553	Sequence 11553, A
98	34	3.1	37	9	US-09-997-653-463	Sequence 463, App	c 171	33	3.0	25	9	US-10-215-112-11554	Sequence 11554, A
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101	34	3.1	37	9	US-09-990-562-463	Sequence 463, App	c 174	33	3.0	25	10	US-09-866-108-3927	Sequence 3927, Ap
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112	34	3.1	37	9	US-09-990-443-463	Sequence 463, App	c 185	33	3.0	25	10	US-09-827-998-939	Sequence 939, App
113	34	3.1	37	9	US-09-990-726-463	Sequence 463, App	c 186	33	3.0	25	10	US-09-827-998-940	Sequence 940, App
114	34	3.1	37	9	US-09-997-559-463	Sequence 463, App	c 187	33	3.0	28	10	US-09-835-381-11	Sequence 11, Appli
115	34	3.1	37	9	US-09-997-601-463	Sequence 463, App	c 188	33	3.0	30	9	US-09-364-847-24	Sequence 24, Appli
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117	34	3.1	37	9	US-09-989-729A-463	Sequence 463, App	c 190	33	3.0	30	10	US-09-738-847-3	Sequence 3, Appli
118	34	3.1	37	9	US-09-990-440-463	Sequence 463, App	c 191	33	3.0	31	9	US-09-912-263-320	Sequence 320, App
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120	34	3.1	37	9	US-09-997-349-463	Sequence 463, App	c 193	33	3.0	31	9	US-09-776-474-2455	Sequence 2455, Ap
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126	34	3.1	37	9	US-09-997-542-463	Sequence 463, App	c 199	33	3.0	32	9	US-10-116-420-30	Sequence 30, Appli
127	34	3.1	37	9	US-09-990-427-463	Sequence 463, App	c 200	33	3.0	33	9	US-09-863-733A-30	Sequence 30, Appli
128	34	3.1	37	9	US-09-990-439-463	Sequence 463, App	c 201	33	3.0	35	9	US-09-837-621-33	Sequence 33, Appli
129	34	3.1	37	9	US-09-989-328-463	Sequence 463, App	c 202	33	3.0	35	10	US-09-788-038-33	Sequence 33, Appli
130	34	3.1	37	9	US-09-993-583-463	Sequence 463, App	c 203	33	3.0	35	10	US-09-975-374A-3	Sequence 3, Appli
131	34	3.1	37	9	US-09-941-992-463	Sequence 463, App	c 204	33	3.0	36	10	US-09-504-231A-1779	Sequence 1779, Ap
132	34	3.1	37	9	US-09-992-521-463	Sequence 463, App	c 205	33	3.0	36	10	US-09-274-553B-1779	Sequence 1779, Ap
133	34	3.1	37	9	US-09-997-333-463	Sequence 463, App	c 206	33	3.0	38	9	US-09-500-700-50	Sequence 50, Appli
134	34	3.1	37	9	US-09-997-384-463	Sequence 463, App	c 207	33	3.0	38	10	US-09-179-536B-136	Sequence 136, App
135	34	3.1	37	10	US-09-989-722-463	Sequence 463, App	c 208	33	3.0	38	10	US-09-765-272-337	Sequence 337, App
136	34	3.1	37	10	US-09-989-723-463	Sequence 463, App	c 209	33	3.0	38	10	US-09-987-456-34	Sequence 34, Appli
137	34	3.1	37	10	US-09-989-279-463	Sequence 463, App	c 210	33	3.0	39	9	US-09-933-180-34	Sequence 34, Appli
138	34	3.1	37	10	US-09-989-727-463	Sequence 463, App	c 211	33	3.0	39	10	US-09-473-872-31	Sequence 31, Appli
139	34	3.1	37	10	US-09-853-033-14	Sequence 14, Appli	c 212	33	3.0	39	10	US-09-987-456-63	Sequence 63, Appli
140	34	3.1	37	10	US-09-989-731-463	Sequence 463, App	c 213	33	3.0	40	9	US-09-892-613C-29	Sequence 29, Appli
141	34	3.1	37	10	US-09-989-732-463	Sequence 463, App	c 214	33	3.0	40	10	US-09-245-802-4	Sequence 4, Appli
142	34	3.1	37	10	US-09-991-073-463	Sequence 463, App	32.5	32.5	2.9	36	9	US-10-185-815-69	Sequence 69, Appli
143	34	3.1	37	10	US-09-990-442-463	Sequence 463, App	c 215	33	2.9	18	9	US-09-800-266A-51	Sequence 51, Appli
144	34	3.1	37	10	US-09-991-163-463	Sequence 463, App	c 216	33	2.9	18	9	US-09-895-007A-51	Sequence 51, Appli
145	34	3.1	37	10	US-09-993-604-463	Sequence 463, App	c 217	33	2.9	18	9	US-10-023-909A-51	Sequence 51, Appli
146	34	3.1	37	10	US-09-990-456-463	Sequence 463, App	c 218	33	2.9	18	9	US-09-835-371-21	Sequence 21, Appli
147	34	3.1	37	10	US-09-989-721-463	Sequence 463, App	c 219	33	2.9	18	9	US-09-920-313-51	Sequence 51, Appli
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149	34	3.1	38	9	US-10-072-438-25	Sequence 25, Appli	c 221	33	2.9	18	9	US-09-888-326-755	Sequence 755, App
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c 224	18	9	US-09-931-732-20	Sequence 20, Appl	c 297	31	10	US-09-939-754-1	Sequence 1, Appl
c 225	18	9	US-09-818-918-55	Sequence 55, Appl	c 298	31	10	US-09-939-832-1	Sequence 1, Appl
c 226	18	9	US-10-112-653-1	Sequence 1, Appl	c 299	31	10	US-09-939-832-1	Sequence 55, Appl
c 227	18	9	US-10-112-653-85	Sequence 85, Appl	c 300	31	10	US-09-827-822-1	Sequence 1, Appl
c 228	18	9	US-10-017-995-1	Sequence 1, Appl	c 301	31	10	US-09-990-080-7	Sequence 7, Appl
c 229	18	9	US-10-017-995-54	Sequence 54, Appl	c 302	31	10	US-09-843-250-47	Sequence 47, Appl
c 230	18	9	US-10-017-995-55	Sequence 55, Appl	c 303	31	10	US-09-837-969A-3	Sequence 3, Appl
c 231	18	9	US-10-017-995-91	Sequence 91, Appl	c 304	31	10	US-09-915-060-46	Sequence 46, Appl
c 232	18	9	US-09-776-479-1	Sequence 1, Appl	c 305	31	10	US-09-915-060-51	Sequence 51, Appl
c 233	18	9	US-09-776-479-54	Sequence 54, Appl	c 306	31	10	US-09-841-321A-3	Sequence 3, Appl
c 234	18	9	US-09-776-479-55	Sequence 55, Appl	c 307	31	10	US-09-978-758-20	Sequence 20, Appl
c 235	18	9	US-09-776-479-91	Sequence 91, Appl	c 308	31	10	US-09-952-060-22	Sequence 22, Appl
c 236	18	9	US-10-002-884A-6	Sequence 6, Appl	c 309	31	10	US-09-377-885A-33	Sequence 33, Appl
c 237	18	9	US-10-300-247-51	Sequence 51, Appl	c 310	31	10	US-09-991-470-7	Sequence 7, Appl
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c 239	18	10	US-09-824-468-59	Sequence 59, Appl	c 312	31	10	US-09-968-851-20	Sequence 20, Appl
c 240	18	10	US-09-824-468-104	Sequence 104, Appl	c 313	31	10	US-09-861-257-69	Sequence 69, Appl
c 241	18	10	US-09-969-373-4373	Sequence 4373, App	c 314	31	10	US-09-848-616-47	Sequence 47, Appl
c 242	18	10	US-09-965-116A-7	Sequence 7, Appl	c 315	31	10	US-10-240-072-4	Sequence 4, Appl
c 243	18	10	US-09-965-116A-77	Sequence 77, Appl	c 316	31	10	US-09-813-380-3	Sequence 3, Appl
c 244	18	10	US-09-965-116A-98	Sequence 98, Appl	c 317	31	10	US-09-813-380-4	Sequence 4, Appl
c 245	18	10	US-09-965-116A-99	Sequence 99, Appl	c 318	31	10	US-09-245-487B-25	Sequence 25, Appl
c 246	20	9	US-10-085-056-12	Sequence 12, Appl	c 319	31	10	US-09-245-487B-27	Sequence 27, Appl
c 247	20	9	US-09-888-326-757	Sequence 757, App	c 320	31	10	US-09-747-377-235	Sequence 235, App
c 248	20	9	US-09-888-326-766	Sequence 766, App	c 321	31	10	US-10-194-594-9	Sequence 9, Appl
c 249	20	9	US-09-932-300-72	Sequence 72, Appl	c 322	31	10	US-09-504-231A-3128	Sequence 3128, App
c 250	20	9	US-10-112-653-81	Sequence 81, Appl	c 323	31	10	US-09-274-553D-3128	Sequence 25, Appl
c 251	20	9	US-10-112-653-102	Sequence 102, App	c 324	31	10	US-09-918-696-25	Sequence 25, Appl
c 252	20	9	US-10-017-995-87	Sequence 87, Appl	c 325	31	10	US-09-888-326-417	Sequence 417, App
c 253	20	9	US-10-017-995-109	Sequence 109, App	c 326	31	10	US-10-112-653-141	Sequence 141, App
c 254	20	9	US-09-776-479-87	Sequence 87, Appl	c 327	31	10	US-10-017-995-148	Sequence 148, App
c 255	20	9	US-09-776-479-109	Sequence 109, App	c 328	31	10	US-09-780-533A-3359	Sequence 3359, App
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c 257	21	10	US-09-765-081-398	Sequence 398, App	c 330	31	10	US-09-308-207-47	Sequence 47, App
c 258	21	10	US-09-817-014-61	Sequence 61, Appl	c 331	31	10	US-09-756-186-12	Sequence 12, Appl
c 259	21	10	US-09-940-185-3361	Sequence 3361, App	c 332	31	10	US-09-473-872-33	Sequence 33, Appl
c 260	25	9	US-09-745-317-41	Sequence 41, Appl	c 333	31	10	US-09-946-175-35	Sequence 35, Appl
c 261	25	9	US-10-215-112-11552	Sequence 11552, A	c 334	31	10	US-09-966-277-29	Sequence 29, Appl
c 262	25	10	US-09-866-108-4386	Sequence 4386, App	c 335	31	10	US-09-918-696-13	Sequence 13, Appl
c 263	25	10	US-09-866-108-4387	Sequence 4387, App	c 336	31	10	US-09-918-696-14	Sequence 14, Appl
c 264	25	10	US-09-866-108-5162	Sequence 5162, App	c 337	31	10	US-09-966-930-29	Sequence 29, Appl
c 265	25	10	US-09-866-108-5163	Sequence 5163, App	c 338	31	10	US-09-245-802-94	Sequence 94, Appl
c 266	25	10	US-09-398-399-11	Sequence 11, Appl	c 339	31	10	US-09-974-974-13	Sequence 13, Appl
c 267	25	10	US-09-899-381-11	Sequence 92, Appl	c 340	31	10	US-10-181-846-121	Sequence 121, App
c 268	25	10	US-10-006-856A-92	Sequence 92, Appl	c 341	31	10	US-09-734-846-29	Sequence 29, Appl
c 269	26	9	US-10-006-818A-92	Sequence 92, Appl	c 342	31	10	US-10-099-275-4	Sequence 4, Appl
c 270	26	9	US-10-015-393A-92	Sequence 92, Appl	c 343	31	10	US-09-904-968A-29	Sequence 29, Appl
c 271	26	9	US-09-946-374-92	Sequence 92, Appl	c 344	31	10	US-09-938-689-53	Sequence 53, Appl
c 272	26	9	US-10-012-121A-92	Sequence 92, Appl	c 345	31	10	US-10-006-856A-90	Sequence 90, Appl
c 273	26	9	US-10-015-869A-92	Sequence 92, Appl	c 346	31	10	US-10-006-818A-90	Sequence 90, Appl
c 274	26	9	US-10-006-116A-92	Sequence 92, Appl	c 347	31	10	US-10-015-393A-90	Sequence 90, Appl
c 275	26	9	US-10-006-117A-92	Sequence 92, Appl	c 348	31	10	US-09-946-374-90	Sequence 90, Appl
c 276	26	9	US-10-013-513A-92	Sequence 92, Appl	c 349	31	10	US-10-012-121A-90	Sequence 90, Appl
c 277	26	9	US-10-017-527A-92	Sequence 92, Appl	c 350	31	10	US-10-015-869A-90	Sequence 90, Appl
c 278	26	9	US-10-007-194A-92	Sequence 92, Appl	c 351	31	10	US-10-006-116A-90	Sequence 90, Appl
c 279	26	9	US-10-013-430A-92	Sequence 92, Appl	c 352	31	10	US-10-013-913A-90	Sequence 90, Appl
c 280	26	9	US-10-011-671A-92	Sequence 92, Appl	c 353	31	10	US-10-017-527A-90	Sequence 90, Appl
c 281	26	9	US-10-012-755A-92	Sequence 92, Appl	c 354	31	10	US-10-007-194A-90	Sequence 90, Appl
c 282	26	9	US-09-345-373-92	Sequence 92, Appl	c 355	31	10	US-10-013-430A-90	Sequence 90, Appl
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c 284	28	10	US-09-853-666-13	Sequence 13, Appl	c 357	31	10	US-10-012-755A-90	Sequence 90, Appl
c 285	28	10	US-09-991-936-51	Sequence 51, Appl	c 358	31	10	US-09-940-244-195	Sequence 195, App
c 286	28	10	US-09-817-387-12	Sequence 12, Appl	c 359	31	10	US-09-949-427-95	Sequence 95, Appl
c 287	30	9	US-09-953-052-50	Sequence 50, Appl	c 360	31	10	US-10-010-802-397	Sequence 397, App
c 288	30	9	US-10-196-793A-40	Sequence 40, Appl	c 361	31	10	US-10-300-616-14	Sequence 14, Appl
c 289	30	10	US-09-804-682-80	Sequence 80, Appl	c 362	31	10	US-10-132-382-17	Sequence 17, Appl
c 290	31	9	US-10-158-895-29	Sequence 29, Appl	c 363	31	10	US-09-940-185-565	Sequence 565, App
c 291	31	9	US-09-939-833-1	Sequence 1, Appl	c 364	31	10	US-10-060-756A-2694	Sequence 2694, App
c 292	31	9	US-09-912-263-108	Sequence 108, App	c 365	31	10	US-10-060-756A-2695	Sequence 2695, App
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c 294	31	10	US-09-801-274-112	Sequence 112, App	c 367	31	10		
c 295	31	10	US-09-801-274-431	Sequence 431, App	c 368	31	10		

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370	31	2.8	25	9	US-10-060-756A-2698	Sequence 2698, Ap	443	31	2.8	33	12	US-10-052-545-3	Sequence 3, Appl
371	31	2.8	25	9	US-10-060-756A-2699	Sequence 2699, Ap	444	31	2.8	34	9	US-10-060-841-37	Sequence 37, Appl
372	31	2.8	25	9	US-10-215-112-855	Sequence 855, App	445	31	2.8	34	9	US-10-093-958-30	Sequence 30, Appl
373	31	2.8	25	9	US-10-215-112-863	Sequence 863, App	446	31	2.8	34	9	US-10-093-958-32	Sequence 32, Appl
374	31	2.8	25	9	US-10-215-112-3003	Sequence 3003, Ap	447	31	2.8	34	9	US-09-848-616-46	Sequence 46, Appl
375	31	2.8	25	9	US-10-215-112-3509	Sequence 3509, Ap	448	31	2.8	35	9	US-09-773-593-10	Sequence 10, Appl
376	31	2.8	25	9	US-10-215-112-3635	Sequence 3635, Ap	449	31	2.8	35	9	US-09-733-042-40	Sequence 40, Appl
377	31	2.8	25	9	US-10-215-112-9820	Sequence 9820, Ap	450	31	2.8	35	9	US-09-376-940-21	Sequence 21, Appl
378	31	2.8	25	9	US-10-215-112-9932	Sequence 9932, Ap	451	31	2.8	35	9	US-10-066-127-21	Sequence 21, Appl
379	31	2.8	25	9	US-09-940-185-4333	Sequence 4333, Ap	452	31	2.8	35	10	US-09-732-618-39	Sequence 39, Appl
380	31	2.8	25	10	US-09-770-720-2	Sequence 2, Appl	453	31	2.8	35	10	US-09-765-272-302	Sequence 302, App
381	31	2.8	25	10	US-09-866-108-3928	Sequence 3928, Ap	454	31	2.8	36	9	US-10-149-121-20	Sequence 20, Appl
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383	31	2.8	25	10	US-09-866-108-3930	Sequence 3930, Ap	456	31	2.8	36	10	US-09-804-733A-18	Sequence 18, Appl
384	31	2.8	25	10	US-09-866-108-4388	Sequence 4388, Ap	457	31	2.8	36	10	US-09-815-837-104	Sequence 104, App
385	31	2.8	25	10	US-09-866-108-4389	Sequence 4389, Ap	458	31	2.8	36	10	US-09-944-411-15	Sequence 15, Appl
386	31	2.8	25	10	US-09-866-108-4390	Sequence 4390, Ap	459	31	2.8	36	10	US-09-759-352-9	Sequence 9, Appl
387	31	2.8	25	10	US-09-866-108-5606	Sequence 5606, Ap	460	31	2.8	37	9	US-09-309-196-71	Sequence 71, Appl
388	31	2.8	25	10	US-09-866-108-5607	Sequence 5607, Ap	461	31	2.8	37	9	US-09-353-354-87	Sequence 87, Appl
389	31	2.8	25	10	US-09-866-108-5608	Sequence 5608, Ap	462	31	2.8	37	9	US-10-125-648-18	Sequence 18, Appl
390	31	2.8	25	10	US-09-866-108-5609	Sequence 5609, Ap	463	31	2.8	37	9	US-09-776-474-1322	Sequence 1922, Ap
391	31	2.8	25	10	US-09-866-108-5610	Sequence 5610, Ap	464	31	2.8	37	9	US-09-776-474-1332	Sequence 1932, Ap
392	31	2.8	25	10	US-09-866-108-11101	Sequence 11101, A	465	31	2.8	37	9	US-09-930-423-2775	Sequence 2775, Ap
393	31	2.8	25	10	US-09-866-108-11102	Sequence 11102, A	466	31	2.8	37	9	US-09-930-423-2775	Sequence 2789, Ap
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396	31	2.8	25	10	US-09-866-108-13839	Sequence 13839, A	469	31	2.8	38	9	US-09-780-533A-2845	Sequence 2845, Ap
397	31	2.8	25	10	US-09-866-108-13840	Sequence 13840, A	470	31	2.8	38	9	US-09-848-754A-5023	Sequence 5023, Ap
398	31	2.8	25	10	US-09-866-108-13841	Sequence 13841, A	471	31	2.8	38	10	US-09-769-864-20	Sequence 20, Appl
399	31	2.8	25	10	US-09-866-108-13917	Sequence 13917, A	472	31	2.8	38	10	US-09-848-164-20	Sequence 20, Appl
400	31	2.8	25	10	US-09-866-108-13918	Sequence 13918, A	473	31	2.8	38	10	US-09-874-547-31	Sequence 31, Appl
401	31	2.8	25	10	US-09-827-998-927	Sequence 927, App	474	31	2.8	38	10	US-09-765-272-382	Sequence 382, App
402	31	2.8	25	10	US-09-827-998-927	Sequence 927, App	475	31	2.8	39	9	US-10-087-993-19	Sequence 19, Appl
403	31	2.8	25	10	US-09-827-998-928	Sequence 928, App	476	31	2.8	39	9	US-09-918-656-17	Sequence 17, Appl
404	31	2.8	25	10	US-09-827-998-928	Sequence 928, App	477	31	2.8	39	9	US-09-918-656-18	Sequence 18, Appl
405	31	2.8	25	10	US-09-827-998-929	Sequence 929, App	478	31	2.8	39	9	US-10-081-347-13	Sequence 13, Appl
406	31	2.8	25	10	US-09-827-998-930	Sequence 930, App	479	31	2.8	39	9	US-10-067-790-47	Sequence 47, Appl
407	31	2.8	25	10	US-09-827-998-931	Sequence 931, App	480	31	2.8	39	9	US-10-067-892-47	Sequence 47, Appl
408	31	2.8	25	10	US-09-827-998-932	Sequence 932, App	481	31	2.8	39	9	US-09-539-382-47	Sequence 47, Appl
409	31	2.8	25	10	US-09-827-998-932	Sequence 932, App	482	31	2.8	39	9	US-10-067-893-47	Sequence 47, Appl
410	31	2.8	26	9	US-09-918-702-17	Sequence 17, Appl	483	31	2.8	39	9	US-10-100-679-8	Sequence 8, Appl
411	31	2.8	27	9	US-10-085-476-3	Sequence 3, Appl	484	31	2.8	39	9	US-10-004-633-26	Sequence 26, Appl
412	31	2.8	28	9	US-10-201-964-5	Sequence 5, Appl	485	31	2.8	39	10	US/09/242	Sequence 21, Appl
413	31	2.8	28	9	US-09-902-460-17	Sequence 17, Appl	486	31	2.8	39	10	US-09-473-872-30	Sequence 30, Appl
414	31	2.8	28	9	US-10-231-426-4	Sequence 4, Appl	487	31	2.8	39	10	US-09-473-872-30	Sequence 30, Appl
415	31	2.8	29	10	US-09-739-451-14	Sequence 14, Appl	488	31	2.8	39	10	US-09-473-872-32	Sequence 32, Appl
416	31	2.8	30	9	US-09-983-657-1	Sequence 1, Appl	489	31	2.8	39	10	US-09-946-175-30	Sequence 30, Appl
417	31	2.8	30	9	US-10-027-199-8	Sequence 8, Appl	490	31	2.8	39	10	US-09-905-999-11	Sequence 11, Appl
418	31	2.8	30	9	US-09-877-336-8	Sequence 8, Appl	491	31	2.8	39	10	US-10-101-392-14	Sequence 14, Appl
419	31	2.8	30	9	US-09-952-060-24	Sequence 24, Appl	492	31	2.8	40	9	US-09-988-626-141	Sequence 141, App
420	31	2.8	30	9	US-10-085-906-11	Sequence 11, Appl	493	31	2.8	40	9	US-10-112-488-61	Sequence 61, Appl
421	31	2.8	30	9	US-10-170-997-8	Sequence 8, Appl	494	31	2.8	40	9	US-09-753-436-30	Sequence 30, Appl
422	31	2.8	30	10	US-09-952-677-3	Sequence 3, Appl	495	31	2.8	40	10	US-10-072-036-29	Sequence 29, Appl
423	31	2.8	31	9	US-10-060-841-32	Sequence 32, Appl	496	31	2.8	40	9	US-09-801-274-879	Sequence 879, App
424	31	2.8	31	9	US-09-780-533A-5449	Sequence 5449, Ap	497	30.5	2.8	31	9	US-09-854-799-8	Sequence 8, Appl
425	31	2.8	31	10	US-09-766-396-13	Sequence 13, Appl	498	30.5	2.8	31	9	US-10-096-373-5	Sequence 5, Appl
426	31	2.8	31	10	US-09-801-274-634	Sequence 634, App	499	30.5	2.8	31	10		
427	31	2.8	31	10	US-09-801-274-680	Sequence 680, App	500	30.5	2.8	31	10		
428	31	2.8	31	10	US-09-801-274-1046	Sequence 1046, Ap							
429	31	2.8	31	12	US-10-062-375-13	Sequence 13, Appl							
430	31	2.8	32	9	US-09-854-356-17	Sequence 17, Appl							
431	31	2.8	32	9	US-10-010-920-54	Sequence 54, Appl							
432	31	2.8	32	9	US-09-957-483-60	Sequence 60, Appl							
433	31	2.8	32	9	US-10-008-721-54	Sequence 54, Appl							
434	31	2.8	32	9	US-10-112-488-56	Sequence 56, Appl							
435	31	2.8	32	10	US-09-814-786-35	Sequence 35, Appl							
436	31	2.8	33	9	US-09-991-496-89	Sequence 89, Appl							
437	31	2.8	33	9	US-10-027-961A-15	Sequence 15, Appl							
438	31	2.8	33	9	US-10-022-832-57	Sequence 57, Appl							
439	31	2.8	33	9	US-10-196-730-9	Sequence 9, Appl							
440	31	2.8	33	9	US-10-252-408-11	Sequence 11, Appl							
441	31	2.8	33	10	US-09-874-923-89	Sequence 89, Appl							

RESULT 1

US-09-970-820-11/c

; Sequence 11, Application US/09970820

; Patent No. US20020170077A1

; GENERAL INFORMATION:

; APPLICANT: FALS, DEAN A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

ALIGNMENTS

ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/970,820
FILING DATE: 05-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-970-820-11

Alignment Scores:
Pred. No.: 1.28e+03 Length: 24
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.99% Indels: 0
DB: 9 Gaps: 0

US-09-970-820-11 (1-205) x US-09-970-820-11 (1-24)

140 AspGlyValAsnTrpGlyArg 146
|||||
Db 23 GATGGGTGAACCTGGGGGAGG 3

RESULT 2
US-09-986-718-11/c
Sequence 11, Application US/09986718
Patent No. US20020178458A1
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/986,718
FILING DATE: 09-No. US20020178458A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,573
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-986-718-11

Alignment Scores:
Pred. No.: 1.28e+03 Length: 24
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.99% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-09-986-718-11 (1-24)

140 AspGlyValAsnTrpGlyArg 146
|||||
Db 23 GATGGGTGAACCTGGGGGAGG 3

RESULT 3
US-09-371-900-11/c
Sequence 11, Application US/09371900
Patent No. US20020137700A1
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/371,900
FILING DATE: 11-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A


```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primers
US-09-931-732-21

Alignment Scores:
Pred. No.: 4.74e+03 Length: 22
Score: 38.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.44% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-09-931-732-21 (1-22)

QY 89 valproProValValHisLeu 95
|||||
DB 2 GTGCCACCTGTGGTCCACCTG 22

RESULT 9
US-09-842-842-2/c
; Sequence 2, Application US/0984842
; Publication No. US2003007752A1
; GENERAL INFORMATION:
; APPLICANT: MORTEN, JOHN EDWARD NORRIS
; TITLE OF INVENTION: METHODS FOR ANALYZING LTC4 SYNTHASE POLYMO
; TITLE OF INVENTION: DIAGNOSTIC USE
; FILE REFERENCE: PLS/009901/0282943
; CURRENT APPLICATION NUMBER: US/09/984,842
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 09/485,636
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: GB 9717766.1
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: PCT/GB98/02468
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-842-842-2

Alignment Scores:
Pred. No.: 6.83e+03 Length: 30
Score: 38.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 3.44% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-09-842-842-2 (1-30)

QY 38 AlaProProGlyAlaAlaProAla 45
|||||
DB 29 GCCCGCGCTGGAGCGCCCGCCGCC 6

RESULT 10
US-09-801-274-943/c
; Sequence 943, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510

```

; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 943
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-943

Alignment Scores:
Pred. No.: 7.09e+03 Length: 31
Score: 38.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.44% Indels: 0
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-801-274-943 (1-31)

QY 40 ProGlyAlaProGly 47
Db 31 CCAGGTCGCTCCACCCCTGGG 8

RESULT 11

US-10-125-635A-370/c

; Sequence 370, Application US/10125635A

; Publication No. US20030039635A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Smithgall, Molly D.

; APPLICANT: Carter, Darrick

; APPLICANT: Cheever, Martin A.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Sutherland, R. Alec

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1

; FILE REFERENCE: 210121.465C7

; CURRENT APPLICATION NUMBER: US/10/125,635A

; CURRENT FILING DATE: 2002-07-19

; NUMBER OF SEQ ID NOS: 461

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 370

; LENGTH: 38

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Primer

US-10-125-635A-370

Alignment Scores:

Pred. No.: 9.01e+03 Length: 38
Score: 38.00 Matches: 7
Percent Similarity: 63.64% Conservative: 0
Best Local Similarity: 63.64% Mismatches: 4
Query Match: 3.44% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-10-125-635A-370 (1-38)

QY 36 GlyAlaProGlyAlaProGly 46

Db 35 GGTCCAGCCTCCGCGCACGCCGCCACCG 3

RESULT 12

US-09-938-864-370/c

; Sequence 370, Application US/09938864

; Publication No. US20030072767A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Smithgall, Molly

; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 370
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-938-864-370

Alignment Scores:
Pred. No.: 9.01e+03 Length: 38
Score: 38.00 Matches: 7
Percent Similarity: 63.64% Conservative: 0
Best Local Similarity: 63.64% Mismatches: 4
Query Match: 3.44% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-09-938-864-370 (1-38)

QY 36 GlyAlaProGlyAlaProGly 46

Db 35 GGTCCAGCCTCCGCGCACGCCGCCACCG 3

RESULT 13

US-09-785-019-370/c

; Sequence 370, Application US/09785019

; Publication No. US20030082196A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Cheever, Martin A.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Smithgall, Molly

; APPLICANT: Moulton, Gus

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Sleath, Paul

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1

; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY

; FILE REFERENCE: 210121.465C4

; CURRENT APPLICATION NUMBER: US/09/785,019

; CURRENT FILING DATE: 2001-02-15

; NUMBER OF SEQ ID NOS: 376

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 370

; LENGTH: 38

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Primer

US-09-785-019-370

Alignment Scores:

Pred. No.: 9.01e+03 Length: 38
Score: 38.00 Matches: 7
Percent Similarity: 63.64% Conservative: 0
Best Local Similarity: 63.64% Mismatches: 4
Query Match: 3.44% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-09-785-019-370 (1-38)

QY 36 GlyAlaAProProGlyAlaAProAlaPro 46
||| ||||| ||| ||| |||
Db 35 GGTCCAGCACCTCCGCCCGCAAGCCGCCACCG 3

RESULT 14

US-10-002-603-370/c
; Sequence 370, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 370
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-002-603-370

Alignment Scores:
Pred. No.: 9,01e+03 Length: 38
Score: 38.00 Matches: 7
Percent Similarity: 63.64% Conservative: 0
Best Local Similarity: 63.64% Mismatches: 4
Query Match: 3.44% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-10-002-603-370 (1-38)

QY 36 GlyAlaAProProGlyAlaAProAlaPro 46
||| ||||| ||| ||| |||
Db 35 GGTCCAGCACCTCCGCCCGCAAGCCGCCACCG 3

RESULT 15

US-09-920-342-11
; Sequence 11, Application US/09920342
; Patent No. US20020137709A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Lin, Shi-lung
; APPLICANT: Chuong, Cheng-Ming
; APPLICANT: Widelitz, Randall B.
; TITLE OF INVENTION: GENE SILENCING USING MRNA-CDNA HYBRIDS
; FILE REFERENCE: 13761-7024
; CURRENT APPLICATION NUMBER: US/09/920,342
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 60/222,479
; PRIOR FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: bcl2 primer
US-09-920-342-11

Alignment Scores:
Pred. No.: 6.64e+03 Length: 24
Score: 37.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.35% Indels: 0
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-920-342-11 (1-24)

QY 177 MetThrGluTyrLeuAsnArg 183
||||| ||||| ||||| |||||
Db 3 ATGACTGAGTACCTGGAACCG 23

RESULT 16

US-10-060-756A-2700
; Sequence 2700, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 2700
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-2700

Alignment Scores:
Pred. No.: 6.97e+03 Length: 25
Score: 37.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 3.35% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-10-060-756A-2700 (1-25)

QY 39 ProProGlyAlaAProAlaPro 46
||||| ||||| ||||| |||||
Db 2 CCTCCAGAGGAGCACCAGGCCA 25

RESULT 17

US-10-060-756A-2701
; Sequence 2701, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667

;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/327,898
;; PRIOR FILING DATE: 2001-10-09
;; NUMBER OF SEQ ID NOS: 4804
;; SOFTWARE: Aeomica Sequence Listing Engine
;; SEQ ID NO 2701
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-756A-2701

Alignment Scores:
Pred. No.: 6.97e+03 Length: 25
Score: 37.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 3.35% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-10-060-756A-2701 (1-25)

Qy 39 ProProGlyAlaAlaProAlaPro 46

Db 1 CCTCCAGGAGGACCCGGAAGCCA 24

RESULT 18

US-09-801-274-1740/c
;; Sequence 1740, Application US/09801274
;; Patent No. US20020032319A1
;; GENERAL INFORMATION:
;; APPLICANT: Cargill, Michele
;; APPLICANT: Ireland, James S.
;; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
;; FILE REFERENCE: 2825.2009-001
;; CURRENT APPLICATION NUMBER: US/09/801,274
;; CURRENT FILING DATE: 2001-03-07
;; PRIOR APPLICATION NUMBER: US 60/187,510
;; PRIOR FILING DATE: 2000-03-07
;; PRIOR APPLICATION NUMBER: US 60/206,129
;; PRIOR FILING DATE: 2000-05-22
;; NUMBER OF SEQ ID NOS: 1802
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1740
;; LENGTH: 31
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-801-274-1740

Alignment Scores:
Pred. No.: 8.98e+03 Length: 31
Score: 37.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.35% Indels: 0
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-801-274-1740 (1-31)

Qy 190 GlnAspAsnGlyGlyTyrPValGly 197
|||||:||||| |||||||

Db 30 CAGGACAGTGGCGGRTGGGTAGGC 7
RESULT 19
US-09-874-503-34/c
;; Sequence 34, Application US/09874503
;; Patent No. US20020177188A1
;; GENERAL INFORMATION:
;; APPLICANT: Chen, Jian
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Li, Hanzhong
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Hymowitz, Sarah G.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Starovasnik, Melissa A.
;; APPLICANT: VanLookeren, Menno
;; APPLICANT: Vandlen, Richard
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Yansura, Daniel
;; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;; FILE REFERENCE: P1381R1C1P3(US)
;; CURRENT APPLICATION NUMBER: US/09/874,503
;; CURRENT FILING DATE: 2001-06-05
;; PRIOR APPLICATION NUMBER: US 60/253,646
;; PRIOR FILING DATE: 2000-11-28
;; PRIOR APPLICATION NUMBER: US 60/244,072
;; PRIOR FILING DATE: 2000-10-26
;; PRIOR APPLICATION NUMBER: US 60/242,837
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: US 60/175,481
;; PRIOR FILING DATE: 2000-01-11
;; PRIOR APPLICATION NUMBER: US 60/191,007
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: US 60/213,807
;; PRIOR FILING DATE: 2000-06-22
;; PRIOR APPLICATION NUMBER: US 60/172,096
;; PRIOR FILING DATE: 1999-12-23
;; PRIOR APPLICATION NUMBER: US 60/138,387
;; PRIOR FILING DATE: 1999-06-09
;; PRIOR APPLICATION NUMBER: US 60/134,287
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: US 60/131,022
;; PRIOR FILING DATE: 1999-04-26
;; PRIOR APPLICATION NUMBER: US 60/130,232
;; PRIOR FILING DATE: 1999-04-21
;; PRIOR APPLICATION NUMBER: US 60/113,621
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: US 60/085,579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: US 09/854,208
;; PRIOR FILING DATE: 2001-05-10
;; PRIOR APPLICATION NUMBER: US 09/854,280
;; PRIOR FILING DATE: 2001-05-20
;; PRIOR APPLICATION NUMBER: US 09/816,744
;; PRIOR FILING DATE: 2001-03-22
;; PRIOR APPLICATION NUMBER: US 09/747,259
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: US 09/644,848
;; PRIOR FILING DATE: 2000-08-22
;; PRIOR APPLICATION NUMBER: US 09/380,142
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: US 09/380,138
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: US 09/311,832
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: US PCT/US01/06520
;; PRIOR FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: US PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US PCT/US00/07532
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US PCT/US99/31274
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: US PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US PCT/US99/05028
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 34
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-874-503-34

Alignment Scores: 9.66e+03 Length: 33
Pred. No.: 37.00 Matches: 6
Score: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.35% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-09-874-503-34 (1-33)

Oy 56 ThrProHisProAlaAlaSerArg 63

Db 25 ACACCCCATCTGTAGCCATCGC 2

RESULT 20

Sequence 34, Application US/10000157
Publication No. US20020182673A1
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul L.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hymowitz, Sarah
APPLICANT: Tumas, Daniel
APPLICANT: Starovasnik, Melissa.
APPLICANT: VanLookeren, Menno
APPLICANT: Vandlen, Richard
APPLICANT: Watanabe, Colin
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William
APPLICANT: Yansura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381R1CIP4 (US)
CURRENT APPLICATION NUMBER: US/10/000,157

CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/138387
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/172096
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/175481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/191007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/213807
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/242837
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/244072
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/253646
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/644848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 09/747259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/816744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/854208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/854280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/874503
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/908827
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/929404
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/931836
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/31274
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/07532
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10

;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
;; PRIOR APPLICATION NUMBER: PCT/US00/34956
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: PCT/US01/17800
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: PCT/US01/19692
;; PRIOR FILING DATE: 2001-06-20
;; PRIOR APPLICATION NUMBER: PCT/US01/21066
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: PCT/US01/21735
;; PRIOR FILING DATE: 2001-07-09
;; NUMBER OF SEQ ID NOS: 39
;; SEQ ID NO 34
;; LENGTH: 33
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-10-000-157-34

Alignment Scores:
Pred. No.: 9.66e+03 Length: 33
Score: 37.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.35% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-10-000-157-34 (1-33)

QY 56 ThrProHisProAlaAlaSerArg 63
DB 25 ACACCCCATCTGTAGCCACTGCG 2

RESULT 21

US-09-747-259-34/c

;; Sequence 34, Application US/09747259
;; Publication No. US20030008815A1
;; GENERAL INFORMATION:
;; APPLICANT: Genentech, Inc.
;; APPLICANT: Chen, Jian
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Li, Hanzhong
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Tumas, Daniel
;; APPLICANT: VanLookeren, Menno
;; APPLICANT: Vandlen, Richard
;; APPLICANT: Watanabe, Colin
;; APPLICANT: Williams, P Mickey
;; APPLICANT: Wood, William
;; APPLICANT: Yansura, Daniel
;; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;; FILE REFERENCE: P1381R1C1P1(US)
;; CURRENT APPLICATION NUMBER: US/09/747,259
;; CURRENT FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: US 09/311,832
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: US 60/172,096
;; PRIOR FILING DATE: 1999-12-23
;; PRIOR APPLICATION NUMBER: PCT/US99/31274
;; PRIOR FILING DATE: 1999-12-30
;; PRIOR APPLICATION NUMBER: US 60/175,481
;; PRIOR FILING DATE: 2000-01-11
;; PRIOR APPLICATION NUMBER: PCT/US00/04341
;; PRIOR FILING DATE: 2000-02-18

;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: 2000-03-02
;; PRIOR APPLICATION NUMBER: US 60/191,007
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: PCT/US00/07532
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: PCT/US00/15264
;; PRIOR FILING DATE: 2000-06-02
;; PRIOR APPLICATION NUMBER: US 60/213,087
;; PRIOR FILING DATE: 2000-06-22
;; PRIOR APPLICATION NUMBER: US 09/644,848
;; PRIOR FILING DATE: 2000-08-22
;; PRIOR APPLICATION NUMBER: PCT/US00/23328
;; PRIOR FILING DATE: 2000-08-24
;; PRIOR APPLICATION NUMBER: US 60/242,837
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: PCT/US00/30873
;; PRIOR FILING DATE: 2000-11-10
;; PRIOR APPLICATION NUMBER: US 60/253,646
;; PRIOR FILING DATE: 2000-11-28
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
;; NUMBER OF SEQ ID NOS: 39
;; SEQ ID NO 34
;; LENGTH: 33
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-747-259-34

Alignment Scores:
Pred. No.: 9.66e+03 Length: 33
Score: 37.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.35% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-09-747-259-34 (1-33)

QY 56 ThrProHisProAlaAlaSerArg 63
DB 25 ACACCCCATCTGTAGCCACTGCG 2

RESULT 22

US-09-908-827-34/c

;; Sequence 34, Application US/09908827
;; Publication No. US20030054442A1
;; GENERAL INFORMATION:
;; APPLICANT: Chen, Jian
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Li, Hanzhong
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Tumas, Daniel
;; APPLICANT: VanLookeren, Menno
;; APPLICANT: Vandlen, Richard
;; APPLICANT: Watanabe, Colin
;; APPLICANT: Williams, P Mickey
;; APPLICANT: Wood, William
;; APPLICANT: Yansura, Daniel
;; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;; FILE REFERENCE: P1381R1C1P1(US)
;; CURRENT APPLICATION NUMBER: US/09/908,827
;; CURRENT FILING DATE: 2001-07-18
;; PRIOR APPLICATION NUMBER: 60/085,579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/113,621

PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/130,232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131,022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/134,287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/138,387
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/172,096
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/175,481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/191,007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/213,807
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/242,837
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/244,072
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 09/311,832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380,138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380,142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/644,848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 09/747,259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/816,744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/854,208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/854,280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/31274
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/07532
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 34
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-908-827-34

Pred. No.: 9.66e+03 Length: 33
Score: 37.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.35% Indels: 0
DB: Gaps: 0
US-09-375-514-22 (1-205) x US-09-908-827-34 (1-33)
QY 56 ThrProHisProAlaAlaSerArg 63
|||||
Db 25 ACACCCATCCTGTAGCCACTCGC 2
RESULT 23
US-09-245-802-71/c
Sequence 71, Application US/09245802
Patent No. US20010049125A1
GENERAL INFORMATION:
APPLICANT: STENMER PH.D., WILLEM P.C.
APPLICANT: LIPSHUTZ, ROBERT J.
TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
NUMBER OF SEQUENCES: 136
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3634
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/245,802
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,502
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05480
FILING DATE: 18-APR-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY, ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 16528J-015410US
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
US-09-245-802-71

Alignment Scores:
Pred. No.: 1.21e+04 Length: 40
Score: 37.00 Matches: 7
Percent Similarity: 70.00% Conservative: 0
Best Local Similarity: 70.00% Mismatches: 3
Query Match: 3.35% Indels: 0
DB: Gaps: 0

US-09-375-514-22 (1-205) x US-09-245-802-71 (1-40)

QY 51 SerGlnProGlyHisThrProHisProAla 60
|||||

Alignment Scores:

Db 37 ACCGAGCCCCGACACCCCGCACACCCGCT 8
RESULT 24
US-09-734-846-34/c
; Sequence 34, Application US/09734846
; Patent No. US20010007025A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, Qingqiang
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0528
; CURRENT APPLICATION NUMBER: US/09/734,846
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/323,743
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-734-846-34
Alignment Scores:
Pred. No.: 6.78e+03 Length: 20
Score: 36.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 3.26% Indels: 0
DB: 10 Gaps: 0
US-09-375-514-22 (1-205) x US-09-734-846-34 (1-20)
QY 190 GlnAspAsnGlyGlyTrp 195
|||:|||||
Db 18 CAGGAGACGGCGGCTGG 1
RESULT 25
US-09-734-847A-45/c
; Sequence 45, Application US/09734847A
; Patent No. US20020049173A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Monia, Brett P.
; APPLICANT: Freir, Susan
; APPLICANT: McKay, Robert
; APPLICANT: Karrias, James G.
; TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation of mRNA F
; FILE REFERENCE: ISPH-0524
; CURRENT APPLICATION NUMBER: US/09/734,847A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-734-847A-45
Alignment Scores:
Pred. No.: 6.78e+03 Length: 20
Score: 36.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 3.26% Indels: 0
DB: 10 Gaps: 0
US-09-375-514-22 (1-205) x US-09-734-847A-45 (1-20)
QY 190 GlnAspAsnGlyGlyTrp 195
|||:|||||
Db 18 CAGGAGACGGCGGCTGG 1
RESULT 26
US-09-911-904-37/c
; Sequence 37, Application US/09911904
; Publication No. US20030096234A1
; GENERAL INFORMATION:
; APPLICANT: Fair, Spencer B.
; APPLICANT: Pickett, Gavin G.
; APPLICANT: Neft, Robin Eileen
; APPLICANT: Dunn, II, Robert Thomas
; TITLE OF INVENTION: CANINE TOXICITY GENES
; FILE REFERENCE: 400742000200
; CURRENT APPLICATION NUMBER: US/09/911,904
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/220,057
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-911-904-37
Alignment Scores:
Pred. No.: 8.82e+03 Length: 25
Score: 36.00 Matches: 5
Percent Similarity: 85.71% Conservative: 1
Best Local Similarity: 71.43% Mismatches: 1
Query Match: 3.26% Indels: 0
DB: 9 Gaps: 0
US-09-375-514-22 (1-205) x US-09-911-904-37 (1-25)
QY 52 GlnProGlyHisThrProHis 58
:::|||||
Db 24 CGTCCATCTCATACTCCACAT 4
RESULT 27
US-09-866-108-4774/c
; Sequence 4774, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 4774
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4774

Alignment Scores: Length: 25
Pred. No.: 8.82e+03 5
Score: 36.00 Matches: 5
Percent Similarity: 83.33% Conservative: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 3.26% Indels: 0
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4774 (1-25)

QY 54 GlyHisThrProHisPro 59
 ||||| |||||
DB 25 GGACATGCTCCTCATCCA 8

RESULT 28
US-09-866-108-4775/c
; Sequence 4775, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 4775
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4775

Alignment Scores: Length: 25
Pred. No.: 8.82e+03 5
Score: 36.00 Matches: 5
Percent Similarity: 83.33% Conservative: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 3.26% Indels: 0
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4775 (1-25)

QY 54 GlyHisThrProHisPro 59
 ||||| |||||
DB 24 GGACATGCTCCTCATCCA 7

RESULT 29
US-09-866-108-4776/c
; Sequence 4776, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664

CURRENT FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/006666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006665
 PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/006566
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006564
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006662

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 4778
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4778

Alignment Scores:
Pred. No.: 8.82e+03 Length: 25
Score: 36.00 Matches: 5
Percent Similarity: 83.33% Conservatives: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 3.26% Indels: 0
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4778 (1-25)

QY 54 GlyHsthrProHisPro 59
||||| |||||||
Db 21 GGACATGCTCCTCATCCA 4

RESULT 32

US-09-866-108-4779/c
; Sequence 4779, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 4779
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4779

Alignment Scores:
Pred. No.: 8.82e+03 Length: 25
Score: 36.00 Matches: 5
Percent Similarity: 83.33% Conservatives: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 3.26% Indels: 0
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4779 (1-25)

QY 54 GlyHsthrProHisPro 59
||||| |||||||
Db 20 GGACATGCTCCTCATCCA 3

RESULT 33

US-09-866-108-4780/c
; Sequence 4780, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752

SOFTWARE: Acomica Sequence Listing Engine

SEQ ID NO 4780

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapiens

US-09-866-108-4780

Alignment Scores:

Pred. No.: 8.82e+03 Length: 25
Score: 36.00 Matches: 5
Percent Similarity: 83.33% Conservative: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 3.26% Indels: 0
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4780 (1-25)

QY 54 GlyHISThrProHisPro 59

Db 19 GGACATGCTCCTCATCCA 2

RESULT 34

US-09-866-108-4781/c

Sequence 4781, Application US/09866108

Patent No. US20020048800A1

GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: JI, Yonggang

APPLICANT: PENN, Sharon G.

APPLICANT: HANZEL, David K.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: ACOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 60/266,860

PRIOR FILING DATE: 2001-02-05

NUMBER OF SEQ ID NOS: 15752

SOFTWARE: Acomica Sequence Listing Engine

SEQ ID NO 4781

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapiens

US-09-866-108-4781

Alignment Scores:

Pred. No.: 8.82e+03 Length: 25
Score: 36.00 Matches: 5
Percent Similarity: 83.33% Conservative: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 3.26% Indels: 0
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4781 (1-25)

QY 54 GlyHISThrProHisPro 59

Db 18 GGACATGCTCCTCATCCA 1

RESULT 35

US-09-817-387-11/c

Sequence 11, Application US/09817387

Patent No. US20010039263A1

GENERAL INFORMATION:

APPLICANT: Max-Debruck-Centrum fur Molekulare Medizin

TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof

FILE REFERENCE: 101195-24

CURRENT APPLICATION NUMBER: US/09/817,387

CURRENT FILING DATE: 2001-03-26

PRIOR APPLICATION NUMBER: DE 197 20 151.2

PRIOR FILING DATE: 1997-05-02

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 11

LENGTH: 28

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: oligonucleotides, linkages between positions 1

OTHER INFORMATION: to 20 are phosphorothioate, linkages between

OTHER INFORMATION: positions 20 to 28 are N3' to N5'

OTHER INFORMATION: phosphoramidates

OTHER INFORMATION: position 28 is modified by a 3'-aminodeoxyribose

OTHER INFORMATION: residue

US-09-817-387-11

Alignment Scores:

Pred. No.: 1.01e+04 Length: 28
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.26% Indels: 0
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-817-387-11 (1-28)

QY 142 ValAsnTrpGlyArgIle 147

Db 18 GTGAAGTGGGGAGGATT 1

RESULT 36

US-09-949-145-28/c

Sequence 28, Application US/09949145

Patent No. US20020055622A1

GENERAL INFORMATION:

APPLICANT: New York Blood Center

TITLE OF INVENTION: Mammalian No. US20020055622A1-erythroid Rh Type C Genes and

FILE REFERENCE: Docket 454-31

CURRENT APPLICATION NUMBER: US/09/949,145

CURRENT FILING DATE: 2001-09-07

PRIOR APPLICATION NUMBER: US 60/230660

PRIOR FILING DATE: 2000-09-07

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.1

SEQ ID NO 28

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1215
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-801-274-1215

Alignment Scores:
Pred. No.: 1.14e+04 Length: 31
Score: 36.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.26% Indels: 0
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-801-274-1215 (1-31)

Qy 72 LeuGlnThrProAlaPro 78

Db 27 CTACAGAGCCGCGGCCCT 7

RESULT 40

US-09-854-356-15/c
; Sequence 15, Application US/09854356
; Patent No. US20020177567A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Gheysen, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: SmithKline Beecham Biologicals S. A.
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-09-854-356-15

Alignment Scores:
Pred. No.: 1.18e+04 Length: 32
Score: 36.00 Matches: 4
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 0
Query Match: 3.26% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-09-854-356-15 (1-32)

Qy 185 LeuHisThrTrpIleGlnAspAsn 192

Db 26 GTGCACACTTGGGTCCGGATCA 3

RESULT 41

US-10-000-512-23/c
; Sequence 23, Application US/10000512
; Patent No. US20020164699A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Fernandes, Elma
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES ENCODING SAME
; FILE REFERENCE: 15966-556
; CURRENT APPLICATION NUMBER: US/10/000,512

; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/619,252
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/167,785
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR PRIMER
US-10-000-512-23

Alignment Scores:
Pred. No.: 1.31e+04 Length: 35
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 3.26% Indels: 0
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-10-000-512-23 (1-35)

Qy 40 ProGlyAlaProAlaPro 46

Db 35 CCCGGGGCTTCCCGTGGGCC 15

RESULT 42

US-09-473-872-31
; Sequence 31, Application US/09473872
; Patent No. US20020064876A1
; GENERAL INFORMATION:
; APPLICANT: Yoon, Kyonggeun
; TITLE OF INVENTION: No. US20020064876A1e1 Gene Therapy Methods For The Treatment
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: JEFF-YO001
; CURRENT APPLICATION NUMBER: US/09/473,872
; CURRENT FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: COL7A1 gene
; OTHER INFORMATION: fragment from a normal human
US-09-473-872-31

Alignment Scores:
Pred. No.: 1.49e+04 Length: 39
Score: 36.00 Matches: 6
Percent Similarity: 60.00% Conservative: 0
Best Local Similarity: 60.00% Mismatches: 4
Query Match: 3.26% Indels: 0
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-473-872-31 (1-39)

Qy 75 ProAlaAlaProGlyAlaAlaAlaGlyPro 84

Db 4 CCAGGGGGTCCCGAGCTCCCGGGGGCCCA 33

RESULT 43

US-09-894-633A-78
; Sequence 78, Application US/09894633A
; Patent No. US20020124285A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy
; APPLICANT: Dubois, Patrice
; APPLICANT: Malven, Marianne

```

: APPLICANT: Masucci, James
: TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL OF GENE EXPRESSION
: FILE REFERENCE: 38-21(15856)B
: CURRENT APPLICATION NUMBER: US/09/894,633A
: CURRENT FILING DATE: 2001-06-28
: PRIOR APPLICATION NUMBER: 60/214,357
: PRIOR FILING DATE: 2000-06-28
: PRIOR APPLICATION NUMBER: 09/894,633
: PRIOR FILING DATE: 2000-06-28
: NUMBER OF SEQ ID NOS: 111
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 78
: LENGTH: 39
: TYPE: DNA
: ORGANISM: artificial sequence
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (1)..(39)
: OTHER INFORMATION: synthetic primer sequence
: IS-09-894-633A-78

```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4465
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4465

Alignment Scores:
Pred. No.: 1.12e+04 Length: 25
Score: 35.00 Matches: 5
Percent Similarity: 83.33% Conservative: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 3.17% Indels: 0
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4465 (1-25)

QY 53 ProglyHsthrProHis 58

Db 25 CCAGGGCACCAGCCCAT 8

RESULT 47

US-09-866-108-4466/c
; Sequence 4466, Application US/09866108

; Patent No. US20020048800A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4466
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4466

Alignment Scores:
Pred. No.: 1.12e+04 Length: 25
Score: 35.00 Matches: 5
Percent Similarity: 83.33% Conservative: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 3.17% Indels: 0
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4466 (1-25)

QY 53 ProglyHsthrProHis 58

Db 24 CCAGGGCACCAGCCCAT 7

RESULT 48

US-09-866-108-4467/c

; Sequence 4467, Application US/09866108

; Patent No. US20020048800A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4467
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4467

Alignment Scores: 1.12e+04 Length: 25
Pred. No.: 35.00 Matches: 5
Score: 83.33% Conservative: 0
Percent Similarity: 83.33% Mismatches: 0
Best Local Similarity: 83.33% Indels: 0
Query Match: 3.17% Gaps: 0
DB: 10

US-09-375-514-22 (1-205) x US-09-866-108-4467 (1-25)

QY 53 ProGlyHisThrProHis 58
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Db 23 CCAGGGCACCAGCCCAT 6

RESULT 49

US-09-866-108-4468/c
; Sequence 4468, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 4468
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4468

Alignment Scores: 1.12e+04 Length: 25
Pred. No.: 35.00 Matches: 5
Score: 83.33% Conservative: 0
Percent Similarity: 83.33% Mismatches: 1
Best Local Similarity: 83.33% Indels: 0
Query Match: 3.17% Gaps: 0
DB: 10

US-09-375-514-22 (1-205) x US-09-866-108-4468 (1-25)

QY 53 ProGlyHisThrProHis 58
|||||
Db 22 CCAGGGCACCAGCCCAT 5

RESULT 50

US-09-866-108-4469/c
; Sequence 4469, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4469
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4469

Alignment Scores:
Pred. No.: 1.12e+04 Length: 25
Score: 35.00 Matches: 5
Percent Similarity: 83.33% Conservative: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 3.17% Indels: 0
DB: 10 Gaps: 0
US-09-375-514-22 (1-205) x US-09-866-108-4469 (1-25)
Qy 53 ProGlyHisThrProHis 58
Db 21 CCAGGGCACCCAGCCCAT 4

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Job time : 134 secs

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Maximum Match 100%
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SUMMARIES

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C 4	55	5.0	24	2	US-08-978-523-8	Sequence 8, Appl	
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C 12	44	4.0	24	2	US-08-599-654-11	Sequence 11, Appl	

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c 91	36	3.3	39	4	US-09-485-737B-6	Sequence 6, Appl	c 165	33.5	3.0	36	3	PCT-US95-10973A-38	Patent No. 5520913
c 92	36	3.3	40	4	US-08-145-704-19	Sequence 19, Appl	c 166	33.5	3.0	36	6	US-08-987-574-48	Sequence 48, Appl
c 93	35.5	3.2	26	1	US-08-535-168-19	Sequence 19, Appl	c 167	33	3.0	16	3	US-08-535-168-48	Sequence 48, Appl
c 94	35.5	3.2	26	3	US-08-987-574-19	Sequence 19, Appl	c 168	33	3.0	16	4	US-09-017-974-48	Sequence 48, Appl
c 95	35.5	3.2	26	4	US-08-535-168-19	Sequence 19, Appl	c 169	33	3.0	16	4	US-08-682-255A-48	Sequence 48, Appl
c 96	35.5	3.2	26	4	US-09-017-974-19	Sequence 19, Appl	c 170	33	3.0	16	4	US-09-429-130-48	Sequence 48, Appl
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c 98	35.5	3.2	26	4	US-09-429-130-19	Sequence 19, Appl	c 172	33	3.0	16	5	PCT-US96-11786-48	Sequence 48, Appl
c 99	35.5	3.2	26	5	PCT-US96-11786-19	Sequence 19, Appl	c 173	33	3.0	17	1	US-08-145-704-33	Sequence 33, Appl
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c 102	35.5	3.2	27	3	US-08-535-168-14	Sequence 14, Appl	c 176	33	3.0	17	3	US-08-987-574-46	Sequence 46, Appl
c 103	35.5	3.2	27	4	US-09-017-974-14	Sequence 14, Appl	c 177	33	3.0	17	4	US-08-535-168-33	Sequence 33, Appl
c 104	35.5	3.2	27	4	US-08-682-255A-14	Sequence 14, Appl	c 178	33	3.0	17	4	US-08-535-168-46	Sequence 46, Appl
c 105	35.5	3.2	27	4	US-09-429-130-14	Sequence 14, Appl	c 179	33	3.0	17	4	US-09-017-974-33	Sequence 33, Appl
c 106	35.5	3.2	27	5	PCT-US96-11786D-13	Sequence 13, Appl	c 180	33	3.0	17	4	US-09-017-974-46	Sequence 46, Appl
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c 108	35	3.2	20	2	US-08-551-211-2	Sequence 2, Appl	c 182	33	3.0	17	4	US-09-017-974-60	Sequence 60, Appl
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c 114	35	3.2	32	1	US-08-726-160-14	Sequence 14, Appl	c 188	33	3.0	17	4	US-08-682-255A-33	Sequence 33, Appl
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c 118	35	3.2	36	5	PCT-US96-07496-8	Sequence 8, Appl	c 192	33	3.0	17	4	US-08-682-255A-60	Sequence 60, Appl
c 119	35	3.2	38	3	US-08-863-813A-49	Sequence 49, Appl	c 193	33	3.0	17	4	US-08-682-255A-68	Sequence 68, Appl
c 120	35	3.2	39	4	US-09-143-634-10	Sequence 10, Appl	c 194	33	3.0	17	4	US-08-682-255A-72	Sequence 72, Appl
c 121	35	3.2	39	4	US-09-593-995-8	Sequence 8, Appl	c 195	33	3.0	17	4	US-08-682-255A-75	Sequence 75, Appl
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c 124	34	3.1	20	4	US-08-545-809A-86	Sequence 86, Appl	c 198	33	3.0	17	4	US-09-429-130-33	Sequence 33, Appl
c 125	34	3.1	20	4	US-07-936-421-6	Sequence 6, Appl	c 199	33	3.0	17	4	US-09-429-130-46	Sequence 46, Appl
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c 133	34	3.1	30	2	US-08-712-610-6	Sequence 6, Appl	c 207	33	3.0	17	4	PCT-US96-11786-46	Sequence 46, Appl
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c 135	34	3.1	30	4	US-09-052-919-51	Sequence 51, Appl	c 209	33	3.0	17	5	US-08-145-704-31	Sequence 31, Appl
c 136	34	3.1	31	1	US-08-530-492-137	Sequence 137, App	c 210	33	3.0	18	1	US-08-319-492B-749	Sequence 749, App
c 137	34	3.1	31	4	US-08-906-517-137	Sequence 137, App	c 211	33	3.0	18	1	US-08-987-574-3	Sequence 3, Appl
c 138	34	3.1	32	2	US-08-174-672D-49	Sequence 49, Appl	c 212	33	3.0	18	1	US-08-987-574-31	Sequence 31, Appl
c 139	34	3.1	33	1	US-08-424-268-2	Sequence 2, Appl	c 213	33	3.0	18	1	US-08-987-574-32	Sequence 32, Appl
c 140	34	3.1	33	2	US-08-967-101-142	Sequence 142, App	c 214	33	3.0	18	1	US-08-535-168-3	Sequence 3, Appl
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c 142	34	3.1	33	3	US-09-124-698-142	Sequence 142, App	c 216	33	3.0	18	4	US-08-535-168-32	Sequence 32, Appl
c 143	34	3.1	33	4	US-09-127-480-142	Sequence 142, App	c 217	33	3.0	18	4	US-09-017-974-3	Sequence 3, Appl
c 144	34	3.1	33	4	US-07-987-264-26	Sequence 26, App	c 218	33	3.0	18	4	US-09-017-974-31	Sequence 31, Appl
c 145	34	3.1	33	4	US-08-496-841C-142	Sequence 142, App	c 219	33	3.0	18	4	US-09-017-974-32	Sequence 32, Appl
c 146	34	3.1	33	4	US-09-124-523-142	Sequence 142, App	c 220	33	3.0	18	4	US-08-682-255A-3	Sequence 3, Appl
c 147	34	3.1	33	5	PCT-US93-10442-2	Sequence 2, Appl	c 221	33	3.0	18	4	US-08-682-255A-31	Sequence 31, Appl
c 148	34	3.1	34	1	US-08-373-124A-31	Sequence 31, Appl	c 222	33	3.0	18	4	US-09-429-130-3	Sequence 3, Appl
c 149	34	3.1	34	1	US-08-435-628-31	Sequence 31, Appl	c 223	33	3.0	18	4	US-09-429-130-31	Sequence 31, Appl
c 150	34	3.1	36	1	US-08-352-179-15	Sequence 15, Appl	c 224	33	3.0	18	4	US-09-429-130-32	Sequence 32, Appl
c 151	34	3.1	36	1	US-08-352-179-16	Sequence 16, Appl	c 225	33	3.0	18	4	PCT-US96-11786-3	Sequence 3, Appl
c 152	34	3.1	38	4	US-09-499-884-12	Sequence 12, Appl	c 226	33	3.0	18	4	PCT-US96-11786-31	Sequence 31, Appl
c 153	34	3.1	39	1	US-08-737-597-7	Sequence 7, Appl	c 227	33	3.0	18	4	PCT-US96-11786-32	Sequence 32, Appl
c 154	34	3.1	39	2	US-09-057-762-5	Sequence 5, Appl	c 228	33	3.0	18	4	PCT-US96-11786-33	Sequence 33, Appl
c 155	34	3.1	39	3	US-08-326-119A-5	Sequence 5, Appl	c 229	33	3.0	18	5	PCT-US96-11786-31	Sequence 31, Appl
c 156	34	3.1	39	4	US-08-513-783A-147	Sequence 147, App	c 230	33	3.0	18	5	PCT-US96-11786-32	Sequence 32, Appl
c 157	34	3.1	39	4	US-09-538-709-36	Sequence 36, Appl	c 231	33	3.0	18	5	PCT-US96-11786-32	Sequence 32, Appl
c 158	34	3.1	39	4	US-09-538-709-37	Sequence 37, Appl							

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237	33	3.0	23	1	US-08-479-156-14	Sequence 14, Appli	310	32.5	2.9	37	4	US-08-433-505-1	Sequence 1, Appli
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c 261	33	3.0	30	2	US-08-117-952-630	Sequence 630, App	334	32	2.9	21	2	US-08-778-794A-145	Sequence 145, App
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c 273	33	3.0	32	1	US-08-061-889-4	Sequence 4, Appli	346	32	2.9	28	4	US-09-225-928-208	Sequence 208, App
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c 286	33	3.0	36	4	US-09-344-700-33	Sequence 33, Appli	359	32	2.9	30	5	PCT-US95-01775-6	Sequence 6, Appli
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303	33	3.0					376	32	2.9	33			
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c 379	32	2.9	33	1	US-08-096-762-117	Sequence 117, App	c 452	32	2.9	40	4	US-08-327-874A-33	Sequence 33, Appl
c 380	32	2.9	33	2	US-08-676-279-8	Sequence 8, Appl	c 453	32	2.9	40	4	US-09-622-540A-15	Sequence 15, Appl
c 381	32	2.9	33	2	US-08-308-865-117	Sequence 117, App	c 454	32	2.9	40	4	US-09-622-540A-15	Sequence 15, Appl
c 382	32	2.9	33	2	US-08-476-176B-46	Sequence 46, Appl	c 455	32	2.9	40	4	US-09-622-540A-15	Sequence 15, Appl
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c 384	32	2.9	33	3	US-08-127-721A-46	Sequence 46, Appl	c 457	31.5	2.9	36	3	US-08-485-133-75	Sequence 75, Appl
c 385	32	2.9	33	3	US-08-485-245A-46	Sequence 46, Appl	c 458	31.5	2.9	36	3	US-08-938-830-58	Sequence 58, Appl
c 386	32	2.9	33	3	US-08-621-841-12	Sequence 12, Appl	c 459	31	2.8	19	1	US-07-936-421-12	Sequence 12, Appl
c 387	32	2.9	33	4	US-08-839-624-34	Sequence 34, Appl	c 460	31	2.8	20	1	US-07-940-242A-94	Sequence 94, Appl
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c 389	32	2.9	33	4	US-08-758-417A-157	Sequence 157, App	c 462	31	2.8	20	1	US-07-940-242A-99	Sequence 99, Appl
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c 392	32	2.9	33	5	PCT-US92-10983-117	Sequence 117, App	c 465	31	2.8	20	4	US-09-490-692-121	Sequence 121, App
c 393	32	2.9	34	1	US-08-318-193-54	Sequence 54, Appl	c 466	31	2.8	20	4	US-09-323-743-29	Sequence 29, Appl
c 394	32	2.9	34	1	US-08-373-124A-32	Sequence 32, Appl	c 467	31	2.8	20	5	PCT-US95-00593-1	Sequence 1, Appl
c 395	32	2.9	34	1	US-08-435-628-32	Sequence 32, Appl	c 468	31	2.8	21	4	US-08-927-219-14	Sequence 14, Appl
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c 397	32	2.9	34	4	US-09-136-574A-11	Sequence 11, Appl	c 470	31	2.8	21	4	US-09-701-685-4	Sequence 4, Appl
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c 399	32	2.9	35	1	US-08-203-078A-2	Sequence 2, Appl	c 472	31	2.8	22	2	US-09-066-597-23	Sequence 23, Appl
c 400	32	2.9	35	1	US-08-217-082A-2	Sequence 2, Appl	c 473	31	2.8	22	3	US-08-466-047B-34	Sequence 34, Appl
c 401	32	2.9	35	2	US-08-465-485A-2	Sequence 2, Appl	c 474	31	2.8	22	3	US-08-247-629-11	Sequence 11, Appl
c 402	32	2.9	35	2	US-08-822-238-3	Sequence 3, Appl	c 475	31	2.8	23	4	US-09-115-446-10	Sequence 10, Appl
c 403	32	2.9	35	3	US-09-080-285-2	Sequence 2, Appl	c 476	31	2.8	23	4	US-08-513-974B-228	Sequence 228, App
c 404	32	2.9	35	3	US-08-892-747-11	Sequence 11, Appl	c 477	31	2.8	24	3	US-08-811-492-41	Sequence 41, Appl
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c 407	32	2.9	36	2	US-08-628-187-1	Sequence 1, Appl	c 480	31	2.8	25	4	US-09-494-407-2	Sequence 2, Appl
c 408	32	2.9	36	2	US-08-811-028-24	Sequence 24, Appl	c 481	31	2.8	25	5	PCT-US96-10545A-41	Sequence 41, Appl
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c 411	32	2.9	36	3	US-08-983-035A-20	Sequence 20, Appl	c 484	31	2.8	26	4	US-08-952-981A-23	Sequence 23, Appl
c 412	32	2.9	36	5	PCT-US95-10973A-38	Sequence 38, Appl	c 485	31	2.8	26	4	US-08-952-981A-23	Sequence 23, Appl
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c 414	32	2.9	37	1	US-08-150-331-30	Sequence 30, Appl	c 487	31	2.8	27	1	US-07-642-734C-20	Sequence 20, Appl
c 415	32	2.9	37	4	US-09-082-649B-49	Sequence 49, Appl	c 488	31	2.8	27	1	US-08-500-857A-17	Sequence 17, Appl
c 416	32	2.9	38	1	US-08-145-704-4	Sequence 4, Appl	c 489	31	2.8	27	3	US-08-439-009A-20	Sequence 20, Appl
c 417	32	2.9	38	1	US-08-384-708A-188	Sequence 188, App	c 490	31	2.8	27	3	US-08-567-200A-36	Sequence 36, Appl
c 418	32	2.9	38	1	US-08-104-072B-34	Sequence 34, Appl	c 491	31	2.8	27	3	US-08-691-794-39	Sequence 39, Appl
c 419	32	2.9	38	1	US-08-642-255-2	Sequence 2, Appl	c 492	31	2.8	27	4	US-08-623-428D-16	Sequence 16, Appl
c 420	32	2.9	38	2	US-08-607-519-2	Sequence 2, Appl	c 493	31	2.8	27	4	US-08-623-428D-16	Sequence 16, Appl
c 421	32	2.9	38	2	US-08-857-946-117	Sequence 117, App	c 494	31	2.8	28	4	US-09-098-628-17	Sequence 17, Appl
c 422	32	2.9	38	3	US-08-970-740-117	Sequence 117, App	c 495	31	2.8	28	4	US-09-098-628-17	Sequence 17, Appl
c 423	32	2.9	38	3	US-08-475-411A-53	Sequence 53, Appl	c 496	31	2.8	28	5	PCT-US91-02186-21	Sequence 21, Appl
c 424	32	2.9	38	3	US-08-987-574-4	Sequence 4, Appl	c 497	31	2.8	29	1	US-08-683-839B-10	Sequence 10, Appl
c 425	32	2.9	38	4	US-08-687-421-188	Sequence 188, App	c 498	31	2.8	29	3	US-09-064-703-16	Sequence 16, Appl
c 426	32	2.9	38	4	US-08-478-029A-53	Sequence 53, Appl	c 499	31	2.8	29	4	US-08-638-931-6	Sequence 6, Appl
c 427	32	2.9	38	4	US-08-535-168-4	Sequence 4, Appl	c 500	31	2.8	30	1	US-08-279-058B-43	Sequence 43, Appl
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c 430	32	2.9	38	4	US-09-429-130-4	Sequence 4, Appl							
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c 433	32	2.9	39	1	US-08-530-492-101	Sequence 101, App							
c 434	32	2.9	39	1	US-08-266-407A-7	Sequence 7, Appl							
c 435	32	2.9	39	2	US-08-892-544-7	Sequence 47, Appl							
c 436	32	2.9	39	3	US-08-968-563-47	Sequence 47, Appl							
c 437	32	2.9	39	3	US-08-969-683A-47	Sequence 17, Appl							
c 438	32	2.9	39	3	US-09-136-605-17	Sequence 101, App							
c 439	32	2.9	39	4	US-08-906-517-101	Sequence 12, Appl							
c 440	32	2.9	39	4	US-08-804-166-12	Sequence 12, Appl							
c 441	32	2.9	39	4	US-08-910-991-12	Sequence 19, Appl							
c 442	32	2.9	39	4	US-09-297-928-19	Sequence 13, Appl							
c 443	32	2.9	40	1	US-08-236-918A-13	Sequence 94, Appl							
c 444	32	2.9	40	2	US-08-425-684-94	Sequence 36, Appl							
c 445	32	2.9	40	2	US-08-628-422-38	Sequence 94, Appl							
c 446	32	2.9	40	2	US-08-675-502-94	Sequence 36, Appl							
c 447	32	2.9	40	4	US-09-416-050A-36	Sequence 36, Appl							
c 448	32	2.9	40	4	US-09-664-800-36	Sequence 36, Appl							
c 449	32	2.9	40	4	US-09-665-309-36	Sequence 36, Appl							
c 450	32	2.9	40	4	US-09-661-569-36	Sequence 36, Appl							

ALIGNMENTS

RESULT 1
US-07-936-421-15
; Sequence 15, Application US/07936421
; Patent No. 5750390
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TREATMENT OF DISEASES CAUSED
; BY EXPRESSION OF THE BCL-2
; TITLE OF INVENTION: GENE
; NUMBER OF INVENTION: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/936,421
FILING DATE: 19920826
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 197/243
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 36
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-936-421-15

Alignment Scores: 29.1 Length: 36
Pred. No.: 66.00 Matches: 11
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 5.98% Gaps: 0
DB: 1

US-09-375-514-22 (1-205) x US-07-936-421-15 (1-36)
Qy 181 LeuAsnArgHisLeuHisThrTrpIleGlnAsp 191
Db 3 CUGACCGGACCCUGACACACCGUGGAGUCCAGGAU 35

RESULT 2
US-07-936-421-5
Sequence 5, Application US/07936421
Patent No. 5750390
GENERAL INFORMATION:
APPLICANT: James D. Thompson
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth G. Draper
TITLE OF INVENTION: METHOD AND REAGENT FOR
TREATMENT OF DISEASES CAUSED
BY EXPRESSION OF THE BCL-2
GENE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/936,421
FILING DATE: 19920826
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

none

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/936,421
FILING DATE: 19920826
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 197/243
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 33
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-936-421-5

Alignment Scores: 164 Length: 33
Pred. No.: 57.00 Matches: 10
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 5.16% Gaps: 0
DB: 1

US-09-375-514-22 (1-205) x US-07-936-421-5 (1-33)
Qy 46 ProGlyIlePheSerGlnProGlyHis 55
Db 3 CCGGCAUCUCCUCCUCCAGCCGCGGCAC 32

RESULT 3
US-08-798-897-8/c
Sequence 8, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA

none

US-08-798-897-8

Alignment Scores:

Pred. No.: 160 Length: 24
Score: 55.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.98% Indels: 0
DB: 1 Gaps: 0

US-09-375-514-22 (1-205) x US-08-798-897-8 (1-24)

QY 188 TptleGlnAspAsnGlyGlyTrp 195

Db 24 TGGATHCARGAAYAYGGNGTGG 1

RESULT 4

US-08-978-523-8/c

Sequence 8, Application US/08978523

Patent No. 5883229

GENERAL INFORMATION:

APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
OPERATING SYSTEM: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/798,897

FILING DATE: February 11, 1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1483.0140002

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

US-08-978-523-8

Alignment Scores:

Pred. No.: 160 Length: 24
Score: 55.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.98% Indels: 0
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-978-523-8 (1-24)

QY 188 TptleGlnAspAsnGlyGlyTrp 195

Db 24 TGGATHCARGAAYAYGGNGTGG 1

Db 24 TGGATHCARGAAYAYGGNGTGG 1

RESULT 5

US-08-217-082A-4

Sequence 4, Application US/08217082A

Patent No. 5734033

GENERAL INFORMATION:

APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716

FILING DATE: 21-FEB-1992

APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Fortney, Andrew D.

REGISTRATION NUMBER: 34,600

REFERENCE/DOCKET NUMBER: 3335-067-55 FWC

TELEPHONE: (408) 436-2070

TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ANTI-SENSE: NO

US-08-217-082A-4

Alignment Scores:

Pred. No.: 1.28e+03 Length: 33
Score: 47.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.26% Indels: 0
DB: 1 Gaps: 0

US-09-375-514-22 (1-205) x US-08-217-082A-4 (1-33)

QY 193 GlyGlyTrpValGlyAlaSerGly 200

Db 10 GGAGCTGGGTAGGTGTCATCTGGT 33

RESULT 6

US-08-465-485A-4

Sequence 4, Application US/08465485A

Patent No. 5831066

GENERAL INFORMATION:

APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29

us-09-375-514-22.rni

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COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/080,285
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/465,485
 FILING DATE: 05-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/124,256
 FILING DATE: 20-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/840,716
 FILING DATE: 21-FEB-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/288,692
 FILING DATE: 22-DEC-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Fortney, Andrew D.
 REGISTRATION NUMBER: 34,600
 REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (408) 436-2070
 TELEFAX: (408) 436-2075
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ANTI-SENSE: NO
 US-09-080-285-4

Alignment Scores:
 Pred. No.: 1.28e+03 Length: 33
 Score: 47.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.26% Indels: 0
 Gaps: 0
 DB:

US-09-375-514-22 (1-205) x US-09-080-285-4 (1-33)
 QY 193 GlyGlyTrpValGlyAlaSerGly 200
 |||||
 Db 10 GGAGGCTGGGTAGTGCATCTGCT 33

RESULT 8
 US-09-724-426-4
 ; Sequence 4, Application US/09724426
 ; Patent No. 6414134
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, John
 ; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
 ; FILE REFERENCE: 10412-024
 ; CURRENT APPLICATION NUMBER: US/09/724,426
 ; CURRENT FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 33
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-724-426-4

Alignment Scores:
 Pred. No.: 1.28e+03 Length: 33
 Score: 47.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.26% Indels: 0
 Gaps: 0
 DB:

CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ADDRESS: P.C.
 STREET: 1755 S. Jefferson Davis Hwy., Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/465,485A
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/124,256
 FILING DATE: 20-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/840,716
 FILING DATE: 21-FEB-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/288,692
 FILING DATE: 22-DEC-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Fortney, Andrew D.
 REGISTRATION NUMBER: 34,600
 REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (408) 436-2070
 TELEFAX: (408) 436-2075
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ANTI-SENSE: NO
 US-08-465-485A-4

Alignment Scores:
 Pred. No.: 1.28e+03 Length: 33
 Score: 47.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.26% Indels: 0
 Gaps: 0
 DB:

US-09-375-514-22 (1-205) x US-08-465-485A-4 (1-33)
 QY 193 GlyGlyTrpValGlyAlaSerGly 200
 |||||
 Db 10 GGAGGCTGGGTAGTGCATCTGCT 33

RESULT 7
 US-09-080-285-4
 ; Sequence 4, Application US/09080285
 ; Patent No. 6040181
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, John
 ; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ADDRESSEE: P.C.
 STREET: 1755 S. Jefferson Davis Hwy., Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.26% Indels: 0
DB: 4 Gaps: 0

US-09-375-514-22 (1-205) x US-09-724-426-4 (1-33)

QY 193 GlycylTrpValGlyAlaSerGly 200
Db 10 GGAGGCTGGTAGTGCATCTGCT 33

RESULT 9

US-07-936-421-8
; Sequence 8, Application US/07936421
; Patent No. 5750390
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: TREATMENT OF DISEASES CAUSED
; TITLE OF INVENTION: BY EXPRESSION OF THE BCL-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/936,421
; FILING DATE: 19920826
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; APPLICATION NUMBER: described below:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/243
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-936-421-8

none

Alignment Scores:
Pred. No.: 1.55e+03 Length: 28
Score: 45.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.08% Indels: 0
DB: 1 Gaps: 0

US-09-375-514-22 (1-205) x US-07-936-421-8 (1-28)

QY 91 ProValHisLeuAlaLeuArgGln 99
Db 1 CCUGUGGUCACCUGCCUCCGCCAA 27

RESULT 10

US-08-480-994-11/c
; Sequence 11, Application US/08480994
; Patent No. 5834248
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,994
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
US-08-480-994-11

Alignment Scores:
Pred. No.: 1.54e+03 Length: 24
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.99% Indels: 0
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-480-994-11 (1-24)

QY 140 AspGlyValAsnTrpGlyArg 146
Db 23 GATGGGTGAACCTGGGGGAGG 3

RESULT 11

US-08-616-844-11/c
; Sequence 11, Application US/08616844
; Patent No. 5849578
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54

us-09-375-514-22.rni

Sun Jun 1 14:56:01 2003

CORRESPONDENCE ADDRESS:
 ADDRESSEE: PENNIE & EDMONDS
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/599,654
 FILING DATE: 09-FEB-1996
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/485,573
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/386,844
 FILING DATE: 10-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: CORUZZI, LAURA A
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-041
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "synthetic oligonucleotide"
 HYPOTHETICAL: NO
 US-08-599-654-11
 Alignment Scores:
 Pred. No.: 1.54e+03
 Score: 44.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 3.99%
 DB: 2
 Length: 24
 Matches: 7
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0
 US-09-375-514-22 (1-205) x US-08-599-654-11 (1-24)
 QY 140 AspGlyValAsnTrpGlyArg 146
 Db 23 GATGGGTGAAGTGGGGGAGG 3
 RESULT 13
 US-08-485-573-11/c
 ; Sequence 11, Application US/08485573
 ; Patent No. 5968770
 ; GENERAL INFORMATION:
 ; APPLICANT: FALB, DEAN A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PENNIE & EDMONDS
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/485,573
 ; FILING DATE: 07-JUN-1995

CORRESPONDENCE ADDRESS:
 ADDRESSEE: PENNIE & EDMONDS
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/616,844
 FILING DATE: 15-MAR-1996
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/599,654
 FILING DATE: 09-FEB-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/485,573
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/386,844
 FILING DATE: 10-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: CORUZZI, LAURA A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-053
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "synthetic oligonucleotide"
 HYPOTHETICAL: NO
 US-08-616-844-11
 Alignment Scores:
 Pred. No.: 1.54e+03
 Score: 44.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 3.99%
 DB: 2
 Length: 24
 Matches: 7
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0
 US-09-375-514-22 (1-205) x US-08-616-844-11 (1-24)
 QY 140 AspGlyValAsnTrpGlyArg 146
 Db 23 GATGGGTGAAGTGGGGGAGG 3
 RESULT 12
 US-08-599-654-11/c
 ; Sequence 11, Application US/08599654
 ; Patent No. 5882925
 ; GENERAL INFORMATION:
 ; APPLICANT: FALB, DEAN A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
 ; NUMBER OF SEQUENCES: 54
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PENNIE & EDMONDS
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA

```
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/386,844
;; FILING DATE: 10-FEB-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CORUZZI, LAURA A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7853-032
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-8864
;; TELE: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
US-08-485-573-11
Alignment Scores:
Pred. No.: 1.54e+03 Length: 24
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.99% Indels: 0
DB: 2 Gaps: 0
US-09-375-514-22 (1-205) x US-08-485-573-11 (1-24)
QY 140 AspGlyValAsnTrpGlyArg 146
Db 23 GATGGGTGAACCTGGGGAGG 3
RESULT 14
US-08-944-868A-11/c
; Sequence 11, Application US/08944868A
; Patent No. 6018025
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,868A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,654
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
```

```
;; TELEFAX: (212) 869-8864
;; TELE: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "synthetic oligonucleotide"
;; HYPOTHETICAL: NO
US-08-944-868A-11
Alignment Scores:
Pred. No.: 1.54e+03 Length: 24
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.99% Indels: 0
DB: 3 Gaps: 0
US-09-375-514-22 (1-205) x US-08-944-868A-11 (1-24)
QY 140 AspGlyValAsnTrpGlyArg 146
Db 23 GATGGGTGAACCTGGGGAGG 3
RESULT 15
US-08-944-423A-11/c
; Sequence 11, Application US/08944423A
; Patent No. 6020463
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,423A
; FILING DATE: 06-OCT-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/599,654
; FILING DATE: 09-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: JUN-07-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELE: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic oligonucleotide"
HYPOTHETICAL: NO
US-08-944-423A-11

Alignment Scores:
Pred. No.: 1.54e+03 Length: 24
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.99% Indels: 0
DB: 3 Gaps: 0

US-09-375-514-22 (1-205) x US-08-944-423A-11 (1-24)

QY 140 AspGlyValAsnTrpGlyArg 146
|||||
DB 23 GATGGGTGAACGGGGGAGG 3

RESULT 16

US-08-925-743-11/c
Sequence 11, Application US/08925743
Patent No. 6054558
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/925,743
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,573
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-032
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
US-08-925-743-11

Alignment Scores:
Pred. No.: 1.54e+03 Length: 24
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.99% Indels: 0

DB: 3 Gaps: 0
US-09-375-514-22 (1-205) x US-08-925-743-11 (1-24)
QY 140 AspGlyValAsnTrpGlyArg 146
|||||
DB 23 GATGGGTGAACGGGGGAGG 3

RESULT 17

US-08-944-496-11/c
Sequence 11, Application US/08944496
Patent No. 6124433
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/944,496
FILING DATE: 06-OCT-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
PRIOR APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-104
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic oligonucleotide"
HYPOTHETICAL: NO
US-08-944-496-11

Alignment Scores:
Pred. No.: 1.54e+03 Length: 24
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.99% Indels: 0
DB: 3 Gaps: 0

US-09-375-514-22 (1-205) x US-08-944-496-11 (1-24)

QY 140 AspGlyValAsnTrpGlyArg 146
|||||

Db 23 GATGGGTGAAGTGGGGAGG 3

RESULT 18
US-08-925-767-11/c
; Sequence 11, Application US/08925767
; Patent No. 6225084
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,767
; FILING DATE: 09-SEPT-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-097
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; S-08-925-767-11

Alignment Scores:
Pred. No.: 1.54e+03 Length: 24
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.99% Indels: 0
DB: 4 Gaps: 0

US-09-375-514-22 (1-205) x US-08-925-767-11 (1-24)

Qy 140 AspGlyValAsnTrpGlyArg 146
; Sequence 596, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert

Db 23 GATGGGTGAAGTGGGGAGG 3

RESULT 19
US-08-859-998-596/c
; Sequence 596, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert

; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 596:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; US-08-859-998-596

Alignment Scores:
Pred. No.: 2.45e+03 Length: 25
Score: 42.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 3.80% Indels: 0
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-859-998-596 (1-25)

Qy 189 IleGlnAspAsnGlyTrpVal 196
; Sequence 596, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert

Db 24 ATCCAAGACCAAGGTGGTGGTG 1
; Sequence 596, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert

RESULT 20
US-09-225-928-596/c
; Sequence 596, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert

; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 596:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 596:
US-09-225-928-596

Alignment Scores: Length: 25
Pred. No.: 2.45e+03
Score: 42.00
Percent Similarity: 87.50%
Best Local Similarity: 87.50%
Query Match: 3.80%
DB: 4

US-09-375-514-22 (1-205) x US-09-225-928-596 (1-25)

Qy 189 IleGlnAspAnGlyGlyTrpVal 196

Db 24 ATCCAAGACCGAGGTGGTG 1

RESULT 21
US-08-440-391-21
; Sequence 21, Application US/08440391
; Patent No. 5656725
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and
; APPLICANT: LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; TITLE OF INVENTION: MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,391
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.147

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-440-391-21

Alignment Scores: Length: 39
Pred. No.: 4.52e+03
Score: 42.00
Percent Similarity: 75.00%
Best Local Similarity: 58.33%
Query Match: 3.80%
DB: 1

US-09-375-514-22 (1-205) x US-08-440-391-21 (1-39)

Qy 101 GlyAspAspPheSerArgArgTyArgGlyAspPhe 112

Db 1 GGGGACGACATCAACCGACGCTATGACTCAGAGTTC 36

RESULT 22
US-08-908-597A-21
; Sequence 21, Application US/08908597A
; Patent No. 5863795
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and
; APPLICANT: LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; TITLE OF INVENTION: MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,597A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,391
; FILING DATE: 12-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-908-597A-21

Alignment Scores: Length: 39
Pred. No.: 4.52e+03
Score: 42.00

Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 58.33% Mismatches: 3
Query Match: 3.80% Indels: 0
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-908-597A-21 (1-39)

Qy 101 GlyAspAspPheSerArgArgTyrArgGlyAspPhe 112
||||||| :||||||| :|||
Db 1 GGGGACGACATCAACCGCGCTATGACTCAGAGTTC 36

RESULT 23

US-09-236-385A-21

; Sequence 21, Application US/09236385A

; Patent No. 6221615

; GENERAL INFORMATION:

; APPLICANT: CHITTENDEN, Thomas D.; and

; LUTZ, Robert J.

; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH

; MODULATE APOPTOSIS

; NUMBER OF SEQUENCES: 41

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hale and Dorr

; CITY: Washington

; STATE: D.C.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/236,385A

; FILING DATE: 25-Jan-1999

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: WIXON, HENRY N.

; REGISTRATION NUMBER: 32,073

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-942-8400

; TELEFAX: 202-942-8400

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 39 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-09-236-385A-21

; Alignment Scores:

Pred. No.: 4.52e+03 Length: 39

Score: 42.00 Matches: 7

Percent Similarity: 75.00% Conservative: 2

Best Local Similarity: 58.33% Mismatches: 3

Query Match: 3.80% Indels: 0

DB: 4 Gaps: 0

US-09-375-514-22 (1-205) x US-09-236-385A-21 (1-39)

Qy 101 GlyAspAspPheSerArgArgTyrArgGlyAspPhe 112

||||||| :||||||| :|||

Db 1 GGGGACGACATCAACCGCGCTATGACTCAGAGTTC 36

RESULT 24

PCT-US96-06122-21

; Sequence 21, Application PC/TUS9606122

; GENERAL INFORMATION:

; APPLICANT: IMMUNOGEN, INC.

; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS

; TITLE OF INVENTION: WHICH MODULATE APOPTOSIS

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hale and Dorr

; CITY: Washington

; STATE: D.C.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/06122

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/440,391

; FILING DATE: 12-MAY-1995

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: WIXON, HENRY N.

; REGISTRATION NUMBER: 32,073

; REFERENCE/DOCKET NUMBER: 104322.147PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-942-8400

; TELEFAX: 202-942-8484

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 39 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

PCT-US96-06122-21

; Alignment Scores:

Pred. No.: 4.52e+03 Length: 39

Score: 42.00 Matches: 7

Percent Similarity: 75.00% Conservative: 2

Best Local Similarity: 58.33% Mismatches: 3

Query Match: 3.80% Indels: 0

DB: 5 Gaps: 0

US-09-375-514-22 (1-205) x PCT-US96-06122-21 (1-39)

Qy 101 GlyAspAspPheSerArgArgTyrArgGlyAspPhe 112

||||||| :||||||| :|||

Db 1 GGGGACGACATCAACCGCGCTATGACTCAGAGTTC 36

RESULT 25

US-08-426-819A-28

; Sequence 28, Application US/08426819A

; Patent No. 5723318

; GENERAL INFORMATION:

; APPLICANT: Yamaguchi, No. 5723318oml

; APPLICANT: Kojima, Tetsuo

; APPLICANT: Oh-Eda, Masayoshi

; APPLICANT: Hattori, Kunihiro

; TITLE OF INVENTION: Genes Coding for Megakaryocyte

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Birch, Stewart, Kolasch & Birch

; STREET: P.O. Box 747

; CITY: Falls Church

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22040-0747

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

us-09-375-514-22.rni

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,819A
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 230-107P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic primer, 850GS"
; S-08-426-819A-28

Alignment Scores:
Pred. No.: 4.41e+03 Length: 33
Score: 41.00 Matches: 8
Percent Similarity: 80.00% Conservative: 0
Best Local Similarity: 80.00% Mismatches: 2
Query Match: 3.71% Indels: 0
Gaps: 0
DB: 1

US-09-375-514-22 (1-205) x US-08-426-819A-28 (1-33)
QY 76 AlaAlaProGlyAlaAlaGlyProAla 85
Db 3 GCGGGCGCTGCTGCCGCTGCGCCAGCC 32

RESULT 26
US-08-427-097-6/c
; Sequence 6, Application US/08427097
; Patent No. 5668294
; GENERAL INFORMATION:
; APPLICANT: Meagher, Richard B.
; APPLICANT: Sommers, Anne O.
; TITLE OF INVENTION: Metal Resistance Sequences and
; TITLE OF INVENTION: Transgenic Plants
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/427,097
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/427,097
; FILING DATE: 21-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 40-94A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
; HYPOTHETICAL: NO
; US-08-878-957-6

Alignment Scores:
Pred. No.: 4.97e+03 Length: 36
Score: 41.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 3.71% Indels: 0
Gaps: 0
DB: 1

US-09-375-514-22 (1-205) x US-08-427-097-6 (1-36)
QY 75 proAlaAlaProGlyAlaAlaAlaGly 83
Db 35 CCTGCTGCGCGGCTGAGGCTGCAGGA 9

RESULT 27
US-08-878-957-6/c
; Sequence 6, Application US/08878957
; Patent No. 5965796
; GENERAL INFORMATION:
; APPLICANT: Meagher, Richard B.
; APPLICANT: Summers, Anne O.
; APPLICANT: Rugh, Clayton L.
; TITLE OF INVENTION: Metal Resistance Sequences and
; TITLE OF INVENTION: Transgenic Plants
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,957
; FILING DATE: 19-JUN-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/427,097
; FILING DATE: 21-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 40-94A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
; HYPOTHETICAL: NO
; US-08-878-957-6

Alignment Scores:
Pred. No.: 4.97e+03 Length: 36
Score: 41.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 3.71% Indels: 0
Gaps: 0
DB: 1

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Score: 41.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 3.71% Indels: 0
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-878-957-6 (1-36)

QY 75 ProAlaProGlyAlaAlaAlaGly 83
Db 35 CCTGCTGCGCGGTGAGCTGCAGGA 9

RESULT 28

US-08-145-704-2/c
; Sequence 2, Application US/08145704
; Patent No. 5567604
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennewald, Susan
; APPLICANT: Zendegeui, Joseph G.
; APPLICANT: Joshua O. Ojwang
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,704
; FILING DATE: 28-OCT-1993
; CLASSIFICATION: 514

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,027
; FILING DATE: 23-APR-1993
; NAME: Paul, Thomas D.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5574-CIP
; TELEPHONE: 713/651-5151
; TELEFAX: 713/651-5246
; TELEX: 762829

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-145-704-2

Alignment Scores:
Pred. No.: 5.36e+03 Length: 38
Score: 41.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 3.71% Indels: 0
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-145-704-2 (1-38)

QY 44 ProAlaProGlyIlePheSerGlnProGlyHisThrProHisPro 59
Db 32 CCCACCCCA-----CCCCCACCACCCACACCC 3

RESULT 29
US-08-987-574-2/c
; Sequence 2, Application US/08987574
; Patent No. 6150339
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennewald, Susan
; APPLICANT: Zendegeui, Joseph G.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/987,574
; FILING DATE:
; CLASSIFICATION: 514

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04529
; FILING DATE: 28-OCT-1993
; APPLICATION NUMBER: US 08/053,027
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5574-CIP
; TELEPHONE: 713/651-5151
; TELEFAX: 713/651-5246
; TELEX: 762829

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-987-574-2

Alignment Scores:
Pred. No.: 5.36e+03 Length: 38
Score: 41.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 3.71% Indels: 0
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-987-574-2 (1-38)

QY 44 ProAlaProGlyIlePheSerGlnProGlyHisThrProHisPro 59
Db 32 CCCACCCCA-----CCCCCACCACCCACACCC 3

RESULT 30

US-08-535-168-2/c
; Sequence 2, Application US/08535168
; Patent No. 6184369
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennewald, Susan

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us-09-375-514-22.rni

APPLICANT: Zendequi, Joseph G.
 APPLICANT: Ojwang, Joshua O.
 APPLICANT: Hogan, Michael E.
 TITLE OF INVENTION: Anti-Viral Guanosine-Rich
 TITLE OF INVENTION: Oligonucleotides
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fulbright & Jaworski
 STREET: 1301 McKinney, Suite 5100
 CITY: Houston
 STATE: Texas
 COUNTRY: U.S.A.
 ZIP: 77010-3095
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/535,168
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04529
 FILING DATE: 28-OCT-1993
 APPLICATION NUMBER: US 08/053,027
 FILING DATE: 23-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Paul, Thomas D.
 REGISTRATION NUMBER: 32,714
 REFERENCE/DOCKET NUMBER: D-5574-CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 713/651-5151
 TELEFAX: 713/651-5246
 TELEX: 762829
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 38 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-535-168-2

Alignment Scores: 5.36e+03 Length: 38
 Pred. No.: 41.00 Matches: 8
 Score: 50.00% Conservative: 0
 Percent Similarity: 50.00% Mismatches: 2
 Best Local Similarity: 50.00% Indels: 6
 Query Match: 3.71% Gaps: 1
 DB:
 US-09-375-514-22 (1-205) x US-08-535-168-2 (1-38)
 QY 44 ProAlaProGlyIlePheSerGlnProGlyHisThrProHisPro 59
 Db 32 CCCACCCCA-----CCCCCCCCACCCACACCCC 3
 RESULT 31
 US-09-017-974-2/c
 ; Sequence 2, Application US/09017974
 ; Patent No. 6288042
 ; GENERAL INFORMATION:
 ; APPLICANT: Rando, Robert F.
 ; APPLICANT: Ojwang, Joshua O.
 ; APPLICANT: Hogan, Michael E.
 ; APPLICANT: Wallace, Thomas L.
 ; APPLICANT: Cossum, Paul A.
 ; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
 ; TITLE OF INVENTION: Tetrad Forming Oligonucleotides
 ; NUMBER OF SEQUENCES: 88
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Conley, Rose & Tayon, P.C.

STREET: 600 Travis, Suite 1800
 CITY: Houston
 STATE: Texas
 COUNTRY: U.S.A.
 ZIP: 77002-2912
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MS Word 97 (saved as .txt file)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/017,974
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/037,374
 FILING DATE: 04-FEB-97
 APPLICATION NUMBER:
 FILING DATE: 09-DEC-97
 ATTORNEY/AGENT INFORMATION:
 NAME: McDaniel, C. Steven
 REGISTRATION NUMBER: 33,962
 REFERENCE/DOCKET NUMBER: 1472-06223
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 713/238-8010
 TELEFAX: 713/238-8008
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 38 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-017-974-2
 Alignment Scores: 5.36e+03 Length: 38
 Pred. No.: 41.00 Matches: 8
 Score: 50.00% Conservative: 0
 Percent Similarity: 50.00% Mismatches: 2
 Best Local Similarity: 50.00% Indels: 6
 Query Match: 3.71% Gaps: 1
 DB:
 US-09-375-514-22 (1-205) x US-09-017-974-2 (1-38)
 QY 44 ProAlaProGlyIlePheSerGlnProGlyHisThrProHisPro 59
 Db 32 CCCACCCCA-----CCCCCCCCACCCACACCCC 3
 RESULT 32
 US-08-682-255A-2/c
 ; Sequence 2, Application US/08682255A
 ; Patent No. 6323185
 ; GENERAL INFORMATION:
 ; APPLICANT: Rando, Robert F.
 ; APPLICANT: Fennewald, Susan
 ; APPLICANT: Zendequi, Joseph G.
 ; APPLICANT: Ojwang, Joshua O.
 ; APPLICANT: Hogan, Michael E.
 ; APPLICANT: Pommier, Yves
 ; APPLICANT: Mazumder, Abhijit
 ; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
 ; TITLE OF INVENTION: Oligonucleotides
 ; NUMBER OF SEQUENCES: 87
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Conley, Rose & Tayon, P.C.
 ; STREET: 600 Travis, Suite 1850
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: U.S.A.
 ; ZIP: 77002-2912
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS Word 97 (saved as .txt file)
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/682,255A
  FILING DATE: 17-JULY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/535,168
  FILING DATE: 23-OCT-95
  APPLICATION NUMBER: 60/001,505
  FILING DATE: 19-JULY-95
  APPLICATION NUMBER: 60/014,007
  FILING DATE: 25-MARCH-96
  APPLICATION NUMBER: 60/013,688
  FILING DATE: 19-MARCH-96
  APPLICATION NUMBER: 60/015,714
  FILING DATE: 17-APRIL-96
  APPLICATION NUMBER: 60/016,271
  FILING DATE: 23-APRIL-96
ATTORNEY/AGENT INFORMATION:
  NAME: McDaniel, C. Steven
  REGISTRATION NUMBER: 33,962
  REFERENCE/DOCKET NUMBER: 1472-06214
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 713/238-8010
    TELEFAX: 713/238-8008
  INFORMATION FOR SEQ ID NO: 2:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 38 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
US-08-682-255A-2

Alignment Scores:
Pred. No.:      5.36e+03      Length:      38
Score:          41.00        Matches:      8
Percent Similarity: 50.00%    Conservative: 0
Best Local Similarity: 50.00%  Mismatches:  2
Query Match:    3.71%        Indels:       6
DB:                                                     Gaps:       1

US-09-375-514-22 (1-205) x US-08-682-255A-2 (1-38)
QY  44 ProAlaProGlyIlePheSerSerGlnProGlyHisThrProHisPro 59
Db  32 CCCACCCCA-----CCCCCCCCACCCACACCCC 3
RESULT 33
US-09-429-130-2/c
Sequence 2, Application US/09429130
Patent No. 6355785
GENERAL INFORMATION:
  APPLICANT: Rando, Robert F.
              Fennewald, Susan
              Zendegeul, Joseph G.
              Ojwang, Joshua O.
              Hogan, Michael E.
              Pommier, Yves
              Mazumder, Abhijit
              60/015,714
  TITLE OF INVENTION: Anti-viral Guanosine-Rich
                    Oligonucleotides
  NUMBER OF SEQUENCES: 87
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Conley, Rose & Tayon, P.C.
    STREET: 600 Travis, Suite 1850
    CITY: Houston
    STATE: Texas
    COUNTRY: U.S.A.
    ZIP: 77002-2912
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS Word 97 (saved as .txt file)
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/429,130
  FILING DATE: 28-Oct-1999
  CLASSIFICATION: <Unknown>
    19-JULY-95
    25-MARCH-96
    19-MARCH-96
    17-APRIL-96
    23-APRIL-96
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/682,255
  FILING DATE: <Unknown>
  APPLICATION NUMBER: 60/001,505
  FILING DATE: 19-JULY-95
  APPLICATION NUMBER: 60/014,007
  FILING DATE: 25-MARCH-96
  APPLICATION NUMBER: 60/013,688
  FILING DATE: 19-MARCH-96
  APPLICATION NUMBER: 60/016,271
  FILING DATE: 17-APRIL-96
ATTORNEY/AGENT INFORMATION:
  NAME: McDaniel, C. Steven
  REGISTRATION NUMBER: 33,962
  REFERENCE/DOCKET NUMBER: 1472-06214
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 713/238-8010
    TELEFAX: 713/238-8008
  INFORMATION FOR SEQ ID NO: 2:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 38 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
    SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-429-130-2

Alignment Scores:
Pred. No.:      5.36e+03      Length:      38
Score:          41.00        Matches:      8
Percent Similarity: 50.00%    Conservative: 0
Best Local Similarity: 50.00%  Mismatches:  2
Query Match:    3.71%        Indels:       6
DB:                                                     Gaps:       1

US-09-375-514-22 (1-205) x US-09-429-130-2 (1-38)
QY  44 ProAlaProGlyIlePheSerSerGlnProGlyHisThrProHisPro 59
Db  32 CCCACCCCA-----CCCCCCCCACCCACACCCC 3
RESULT 34
PCT-US92-09202-10/c
Sequence 10, Application PC/TUS9209202
GENERAL INFORMATION:
  APPLICANT: Hogan, Michael E.
  TITLE OF INVENTION: Triplex Forming Oligonucleotide Reagents Targeted
  TO THE NEU ONCOGENE PROMOTER AND METHOD OF USE
  NUMBER OF SEQUENCES: 10
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fulbright & Jaworski
    STREET: 1301 McKinney, Suite 5100
    CITY: Houston
    STATE: Texas
    COUNTRY: U.S.A.
    ZIP: 77010-3095
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
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us-09-375-514-22.rni

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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09202
; FILING DATE: 19921028
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5393
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5151
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; MOLECULE TYPE: Triplex forming oligonucleotide
; HYPOTHETICAL: YES
; PCT-US92-09202-10

Alignment Scores:
Pred. No.: 5.36e+03 Length: 38
Score: 41.00 Matches: 8
Percent Similarity: 50.00% Conservatives: 0
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 3.71% Indels: 6
DB: 5 Gaps: 1

US-09-375-514-22 (1-205) x PCT-US92-09202-10 (1-38)
Qy 44 ProAlaProGlyIlePheSerGlnProGlyHisThrProHisPro 59
Db 32 CCCACCCCA-----CCCCCCCCACACCCACACCCC 3

RESULT 35
PCT-US93-08329-11/c
; Sequence 11, Application PC/TUS9308329
; GENERAL INFORMATION:
; APPLICANT: Tsai, Ming-Jer
; APPLICANT: Hogan, Michael H
; APPLICANT: O'Malley, Bert W
; APPLICANT: Ing, Nancy H
; TITLE OF INVENTION: Novel Triplex Forming Oligonucleotides
; TITLE OF INVENTION: and Methods for their use
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski Patent Department
; STREET: 1301 McKinney #5100
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08329
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,168; 60/001,505; 60/014,007; 60/013,688;
; APPLICATION NUMBER: 60/015,714; 60/016,271
; FILING DATE: 23-OCT-95; 17-JULY-96; 25-MARCH-96; 23-
; FILING DATE: APRIL-96; 17-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PCT-US93-08329-11

Alignment Scores:
Pred. No.: 5.36e+03 Length: 38
Score: 41.00 Matches: 8
Percent Similarity: 50.00% Conservatives: 0
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 3.71% Indels: 6
DB: 5 Gaps: 1

US-09-375-514-22 (1-205) x PCT-US93-08329-11 (1-38)
Qy 44 ProAlaProGlyIlePheSerGlnProGlyHisThrProHisPro 59
Db 32 CCCACCCCA-----CCCCCCCCACACCCACACCCC 3

RESULT 36
PCT-US96-11786-2/c
; Sequence 2, Application PC/TUS9611786
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennwald, Susan
; APPLICANT: Zendegeui, Joseph G.
; APPLICANT: O'wang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Pommier, Yves
; APPLICANT: Kazunder, Abhijit
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11786
; FILING DATE: 17-JULY-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,168; 60/001,505; 60/014,007; 60/013,688;
; APPLICATION NUMBER: 60/015,714; 60/016,271
; FILING DATE: 23-OCT-95; 17-JULY-96; 25-MARCH-96; 23-
; FILING DATE: APRIL-96; 17-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

MOLECULE TYPE: DNA (genomic)
PCT-US96-11786-2

Alignment Scores:
Pred. No.: 5,36e+03 Length: 38
Score: 41.00 Matches: 8
Percent Similarity: 50.00% Conservativity: 0
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 3.71% Indels: 6
DB: 5 Gaps: 1

US-09-375-514-22 (1-205) x PCT-US96-11786-2 (1-38)

Qy 44 ProAlaproglyIlePheSerGlnProGlyHsThrProHisPro 59
Db 32 CCCACCCCA-----CCCCCAGACACCCACACCC 3

RESULT 37

PCT-US95-06987-10/c

Sequence 10, Application PC/TUS9506987

GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
TITLE OF INVENTION: The Inhibition of Cytokine Production by
TITLE OF INVENTION: Oligonucleotides and Inhibition of Tumors Which are
TITLE OF INVENTION: Responsive to Cytokine Factors
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: US

ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06987
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5669
TELEPHONE: 713/651-5151
TELEFAX: 713/651-5246
TELEX: 762829

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US95-06987-10

Alignment Scores:
Pred. No.: 4,11e+03 Length: 27
Score: 40.00 Matches: 6
Percent Similarity: 85.71% Conservativity: 0
Best Local Similarity: 85.71% Mismatches: 1
Query Match: 3.62% Indels: 0
DB: 5 Gaps: 0

US-09-375-514-22 (1-205) x PCT-US95-06987-10 (1-27)

Qy 53 ProGlyHsThrProHisPro 59

Db 21 CCCACACACACCCACCCCA 1

RESULT 38

US-08-497-312-8
Sequence 8, Application US/08497312
Patent No. 5712120

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Method for obtaining modified

TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine

TITLE OF INVENTION: antibody variable domains, compositions containing them.

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR

STREET: 215 Y 15, ATABEY PLAYA

CITY: HAVANA

STATE:

COUNTRY: CUBA

ZIP: 11600

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/497,312

FILING DATE: 30-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: CU 80/94

FILING DATE: 30-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: BOND, LAURENCE B.

REGISTRATION NUMBER: 30,549

REFERENCE/DOCKET NUMBER: 2629US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 801/532-1922

TELEFAX: 801/531-9168

TELEX: 388961 1PM04UT

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

US-08-497-312-8

Alignment Scores:

Pred. No.: 5,87e+03 Length: 35
Score: 40.00 Matches: 7
Percent Similarity: 80.00% Conservativity: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 3.62% Indels: 0
DB: 1 Gaps: 0

US-09-375-514-22 (1-205) x US-08-497-312-8 (1-35)

Qy 45 AlaProGlyIlePheSerGlnProGly 54

Db 4 GCCCCAGGCTTCTTCACITTCAGCCCCAGGC 33

RESULT 39

US-08-497-312-10/c

Sequence 10, Application US/08497312

Patent No. 5712120

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Method for obtaining modified

TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine

TITLE OF INVENTION: antibody variable domains, compositions containing them.

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR

STREET: 215 Y 15, ATABEY PLAYA
CITY: HAVANA
STATE: CUBA
COUNTRY: CUBA
ZIP: 11600
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,312
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CU 80/94
FILING DATE: 30-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOND, LAURENCE B.
REGISTRATION NUMBER: 30,549
REFERENCE/DOCKET NUMBER: 2629US
TELEPHONE: 801/532-1922
TELEFAX: 801/531-9168
TELEX: 388961 1PM04UT
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-08-497-312-10
Alignment Scores:
Pred. No.: 6.11e+03 Length: 36
Score: 40.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 3.62% Indels: 0
DB: 1 Gaps: 0
US-09-375-514-22 (1-205) x US-08-497-312-10 (1-36)
Qy 45 AlaProGlyIlePheSerSerGlnProGly 54
Db 32 GCCCAGGCTTCTTCACTTCAGCCCCAGGC 3
RESULT 40
US-08-463-682-7
Sequence 7, Application US/08463682
Patent No. 6008193
GENERAL INFORMATION:
APPLICANT: Leonard Garfinkel, et al.
TITLE OF INVENTION: Cloning and Production of Human Von
Willebrand Factor GPIIb Binding Domain Polypeptides and
Methods of Using Same
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,682
FILING DATE: 05-JUN-1995

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 36537-B2-Y
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-463-682-7
Alignment Scores:
Pred. No.: 7.06e+03 Length: 40
Score: 40.00 Matches: 6
Percent Similarity: 85.71% Conservative: 0
Best Local Similarity: 85.71% Mismatches: 1
Query Match: 3.62% Indels: 0
DB: 3 Gaps: 0
US-09-375-514-22 (1-205) x US-08-463-682-7 (1-40)
Qy 53 ProGlyHisThrProHisPro 59
Db 1 CCAGGACGAGCGCCACATCCA 21
RESULT 41
US-08-469-318-110/c
Sequence 110, Application US/08469318
Patent No. 6022535
GENERAL INFORMATION:
APPLICANT: Multivariant IL-3 Hematopoiesis Fusion
TITLE OF INVENTION: Protein
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,318
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,872
FILING DATE:
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-08-469-318-110
Alignment Scores:
Pred. No.: 8.67e+03 Length: 40
Score: 39.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 3.53% Indels: 0
DB: 3 Gaps: 0
US-09-375-514-22 (1-205) x US-08-469-318-110 (1-40)

QY 84 ProAlaLeuSerProValProPro 91
DB 38 CCTGCCATGGCTCCAGTACCACCA 15

RESULT 42

US-08-468-609A-110/c
; Sequence 110, Application US/08468609A
; Patent No. 6030812
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mair H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-3)
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468.609A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/3
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"

US-08-468-609A-110
Alignment Scores:
Pred. No.: 8.67e+03 Length: 40
Score: 39.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 3.53% Indels: 0
DB: 3 Gaps: 0

US-09-375-514-22 (1-205) x US-08-468-609A-110 (1-40)

QY 84 ProAlaLeuSerProValProPro 91
DB 38 CCTGCCATGGCTCCAGTACCACCA 15

RESULT 43

US-08-446-872A-110/c
; Sequence 110, Application US/08446872A
; Patent No. 6361977
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mair H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.872A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/1
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"

US-08-446-872A-110
Alignment Scores:
Pred. No.: 8.67e+03 Length: 40
Score: 39.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 3.53% Indels: 0
DB: 4 Gaps: 0

US-09-375-514-22 (1-205) x US-08-446-872A-110 (1-40)

QY 84 ProAlaLeuSerProValProPro 91
DB 38 CCTGCCATGGCTCCAGTACCACCA 15

RESULT 44

US-08-762-227A-110/c
; Sequence 110, Application US/08762227A
; Patent No. 5436387

APPLICANT:

```
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-485-636-2

Alignment Scores:
Pred. No.: 7.17e+03 Length: 30
Score: 38.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 3.44% Indels: 0
DB: 4 Gaps: 0

US-09-375-514-22 (1-205) x US-09-485-636-2 (1-30)

QY 38 AlaProGlyAlaAlaProAla 45
|||||
Db 29 GCCCGCGCTGGAGCGCCCGCGCC 6

RESULT 47
PCT-US95-06987-3
; Sequence 3, Application PC/TUS9506987
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; TITLE OF INVENTION: The Inhibition of Cytokine Production by
; TITLE OF INVENTION: Oligonucleotides and Inhibition of Tumors which are
; NUMBER OF SEQUENCES: 10 Responsive to Cytokine Factors
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: US
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: PCT/US95/06987
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5669
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5151
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-06987-3

Alignment Scores:
Pred. No.: 8.82e+03 Length: 35
Score: 38.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 3.44% Indels: 0
DB: 5 Gaps: 0

US-09-375-514-22 (1-205) x PCT-US95-06987-3 (1-35)

QY 55 HistHrProHisProAlaAlaSer 62
|||||
Db 9 CACACTCCCATCCTCCTCCTCCTC 32

RESULT 48
US-09-367-750-5
; Sequence 5, Application US/09367750
; Patent No. 6436639
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Ossina, Natalya K.
; TITLE OF INVENTION: BAK PROMOTER EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LXR BIOTECHNOLOGY INC.
; STREET: 3095 Richmond Parkway, Suite 213
; CITY: Richmond
; STATE: CA
; COUNTRY: USA
; ZIP: 94806
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/367,750
; FILING DATE: 07-DEC-1999
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Theresa A.
; REGISTRATION NUMBER: 32,547
; REFERENCE/DOCKET NUMBER: 4147-14-PUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-367-750-5

Alignment Scores:
Pred. No.: 9.17e+03 Length: 36
Score: 38.00 Matches: 6
Percent Similarity: 70.00% Conservative: 1
Best Local Similarity: 60.00% Mismatches: 3
Query Match: 3.44% Indels: 0
DB: 4 Gaps: 0

US-09-375-514-22 (1-205) x US-09-367-750-5 (1-36)

QY 135 GluGluLeuPheArgAspGlyValAsnTrp 144
|||||
Db 7 GAATTCCTGTTTGAGAGTGCGCAATTGG 36

RESULT 49
US-08-217-082A-3/C
; Sequence 3, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 224 Airport Parkway
; CITY: San Jose
; STATE: California
```


us-09-375-514-22.rni

Sun Jun 1 14:56:01 2003

COUNTRY: U.S.A.
 ZIP: 95110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/217,082A
 FILING DATE: 24-MAR-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/840,716
 FILING DATE: 21-FEB-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/288,692
 FILING DATE: 22-DEC-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Fortney, Andrew D.
 REGISTRATION NUMBER: 34,600
 REFERENCE/DOCKET NUMBER: 3335-070-55 FWC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (408) 436-2070
 TELEFAX: (408) 436-2075
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: Synthetic DNA
 ANTI-SENSE: YES
 US-08-217-082A-3

Alignment Scores:
 Pred. No.: 5.04e+03 Length: 20
 Score: 37.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.35% Indels: 0
 DB: 1 Gaps: 0

US-09-375-514-22 (1-205) x US-08-217-082A-3 (1-20)

Qy 193 GlyGlyTrpValGlyAla 198
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 Db 20 GGAGGCTGGGTAGGTGCA 3

RESULT 50
 US-08-465-485A-3/c
 Sequence 3, Application US/08465485A
 Patent No. 5831066
 GENERAL INFORMATION:
 APPLICANT: Reed, John
 TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: P.C.
 STREET: 1755 S. Jefferson Davis Hwy., Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/465,485A
 FILING DATE: 05-JUN-1995

Search completed: May 31, 2003, 23:23:16
 Job time : 67 secs

Alignment Scores:
 Pred. No.: 5.04e+03 Length: 20
 Score: 37.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.35% Indels: 0
 DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-465-485A-3 (1-20)

Qy 193 GlyGlyTrpValGlyAla 198
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 Db 20 GGAGGCTGGGTAGGTGCA 3

us-09-375-514-22.rge

Sun Jun '1 14:55:59 2003

GenCore version 5.1.5
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 31, 2003, 18:42:35 ; Search time 1764 Seconds

(without alignments)
3382.129 Million cell updates/sec

Title: US-09-375-514-22

Sequence: 1104
1 MAHAGRTGYDREIVMYIH.....HTWIQDNGWVGASGDVSLG 205

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 770742

Minimum DB seq length: 10
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Command line parameters: -DEV=slp
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-DB=GenEmbl -QFMT=fastap -SUFFIX=rgc -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=500
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL
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-NO_XLPAY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:
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41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
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C 2	71	6.4	39	6	AX377551 Sequence
C 3	66	6.0	36	6	AR007301 Sequence
C 4	63	5.7	39	6	AX377552 Sequence
C 5	57	5.2	33	6	AR007291 Sequence
C 6	55	5.0	24	6	AR020782 Sequence
C 7	47	4.3	33	6	AR052606 Sequence
C 8	47	4.3	33	6	196085 Sequence 4
C 9	45	4.1	28	6	AR007294 Sequence
C 10	45	4.1	36	9	HSAJ5138 Homo sapi
C 11	44	4.0	24	6	AR053546 Sequence
C 12	44	4.0	24	6	AR065873 Sequence
C 13	44	4.0	24	6	AR080355 Sequence
C 14	44	4.0	24	6	AR148310 Sequence
C 15	43	3.9	28	6	AX031294 Sequence
C 16	43	3.9	28	13	AX031320 Sequence
C 17	42	3.8	25	6	AR090476 Sequence
C 18	42	3.8	25	6	AR197511 Sequence
C 19	42	3.8	39	6	I60569 Sequence 21
C 20	41	3.7	31	6	AX022526 Sequence
C 21	41	3.7	31	6	AX030814 Sequence
C 22	41	3.7	33	6	I89980 Sequence 28
C 23	41	3.7	33	9	S80834 gamma delta
C 24	41	3.7	36	6	I65770 Sequence 6
C 25	41	3.7	38	6	AR168776 Sequence
C 26	41	3.7	38	6	AR200245 Sequence
C 27	41	3.7	38	6	I27770 Sequence 2
C 28	40	3.6	35	6	A47631 Sequence 8
C 29	40	3.6	35	6	I82275 Sequence 10
C 30	40	3.6	36	6	A47633 Sequence 16
C 31	40	3.6	36	6	A68670 Sequence 10
C 32	40	3.6	36	6	I82277 Sequence 10
C 33	40	3.6	40	6	AR096669 Sequence
C 34	40	3.6	40	6	AX262441 Sequence
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C 38	39	3.5	31	6	AX080990 Sequence
C 39	38.5	3.5	31	6	AX248293 Sequence
C 40	38	3.4	20	6	AX224988 Sequence
C 41	38	3.4	24	6	AX224989 Sequence
C 42	38	3.4	24	6	AX113808 Sequence 2
C 43	38	3.4	30	6	A98608 Sequence 2
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C 46	38	3.4	31	6	AX477731 Sequence
C 47	38	3.4	31	6	AX477732 Sequence 10
C 48	38	3.4	33	6	A36722 Sequence 10
C 49	38	3.4	38	6	AX247606 Sequence
C 50	37	3.4	20	6	AR052605 Sequence

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c 52	37	3.4	24	6	AX427162	AX427162 Sequence	c 125	35	3.2	37	6	AR065290
c 53	37	3.4	24	6	E37751	E37751 Process for	c 126	35	3.2	37	6	A39784
c 54	37	3.4	28	6	AR005121	AR005121 Sequence	c 127	35	3.2	37	6	AX175328
c 55	37	3.4	28	6	AR058248	AR058248 Sequence	c 128	35	3.2	37	6	AX175328
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c 57	37	3.4	31	6	AX249661	AX249661 Sequence	c 130	35	3.2	38	6	AR117910
c 58	37	3.4	33	6	AX180797	AX180797 Sequence	c 131	35	3.2	39	6	AX067855
c 59	37	3.4	34	6	AX468208	AX468208 Sequence	c 132	34.5	3.1	37	6	AX080605
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c 62	37	3.4	38	6	AR200244	AR200244 Sequence	c 135	34	3.1	20	6	AR144337
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c 64	37	3.4	40	6	AR053647	AR053647 Sequence	c 137	34	3.1	22	6	AR118073
c 65	37	3.4	40	6	AR112703	AR112703 Sequence	c 138	34	3.1	22	6	AR118074
c 66	37	3.4	40	6	I86248	I86248 Sequence 2	c 139	34	3.1	24	6	AX290177
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c 92	36	3.3	38	6	I15444	I15444 Sequence 22	c 165	34	3.1	26	6	AX042445
c 93	36	3.3	39	6	AR179155	AR179155 Sequence	c 166	34	3.1	26	6	AX042445
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c 114	35	3.2	30	6	AX317336	AX317336 Sequence	c 187	34	3.1	26	6	AX042445
c 115	35	3.2	30	6	E09807	E09807 Mutation pr	c 188	34	3.1	26	6	AX042445
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c 156	35	3.2	33	6	AX030812	AX030812 Sequence	c 229	34	3.1	26	6	AX042445
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c 201	33.5	3.0	40	6	AX168014	AX168014 Sequence	c 274	33	3.0	30	6	AX139036	Sequence
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209	33	3.0	17	6	AR168833	AR168833 Sequence	282	33	3.0	31	6	AR053746	Sequence
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211	33	3.0	17	6	AR168842	AR168842 Sequence	284	33	3.0	31	6	AR178200	Sequence
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221	33	3.0	17	6	AR200311	AR200311 Sequence	c 294	33	3.0	31	6	AX254368	Sequence
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232	33	3.0	18	6	AR200275	AR200275 Sequence	c 305	33	3.0	31	6	AX210344	Sequence
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235	33	3.0	18	6	I39711	I39711 Sequence 74	c 308	33	3.0	31	6	AX210344	Sequence
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237	33	3.0	20	6	AX147401	AX147401 Sequence	310	33	3.0	31	6	AX210344	Sequence
238	33	3.0	21	6	A46336	A46336 Sequence 7	311	33	3.0	31	6	AX210344	Sequence
239	33	3.0	21	6	A46337	A46337 Sequence 8	312	33	3.0	31	6	AX210344	Sequence
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242	33	3.0	22	6	AR067587	AR067587 Sequence	315	33	3.0	31	6	AX210344	Sequence
243	33	3.0	22	6	I32323	I32323 Sequence 4	316	33	3.0	31	6	AX210344	Sequence
244	33	3.0	23	6	I17099	I17099 Sequence 14	317	33	3.0	31	6	AX210344	Sequence
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249	33	3.0	25	6	AX476209	AX476209 Sequence	c 322	33	3.0	31	6	AX210344	Sequence
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263	33	3.0	27	6	I27802	I27802 Sequence 34	c 336	33	3.0	31	6	AX210344	Sequence
264	33	3.0	27	6	I60572	I60572 Sequence 27	c 337	33	3.0	31	6	AX210344	Sequence
265	33	3.0	27	6	I71202	I71202 Sequence 54	c 338	33	3.0	31	6	AX210344	Sequence
266	33	3.0	27	6	I83761	I83761 Sequence 54	c 339	33	3.0	31	6	AX210344	Sequence
267	33	3.0	28	6	AR173104	AR173104 Sequence	c 340	33	3.0	31	6	AX210344	Sequence
268	33	3.0	29	6	AR085809	AR085809 Sequence	c 341	33	3.0	31	6	AX210344	Sequence
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343	6	AR052624	Sequence	32	2.9	18	6	AR052624	Sequence	416	32	2.9	28	6	AR099199	Sequence
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345	18	AR140496	Sequence	32	2.9	18	6	AR140496	Sequence	418	32	2.9	28	6	AR154293	Sequence
346	18	AR146347	Sequence	32	2.9	18	6	AR146347	Sequence	419	32	2.9	28	6	AR197123	Sequence
347	18	AR146392	Sequence	32	2.9	18	6	AR146392	Sequence	420	32	2.9	28	6	AR197415	Sequence
348	18	AR154716	Sequence	32	2.9	18	6	AR154716	Sequence	421	32	2.9	29	6	IO1627	Sequence 4
349	18	AR167448	Sequence	32	2.9	18	6	AR167448	Sequence	422	32	2.9	29	6	IO7502	Sequence 2
350	18	AR015198	Sequence	32	2.9	18	6	AR015198	Sequence	423	32	2.9	29	6	S43673	NADH dehydr
351	18	AX020948	Sequence	32	2.9	18	6	AX020948	Sequence	424	32	2.9	30	6	AX11495	Nucleotide
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354	18	AX040403	Sequence	32	2.9	18	6	AX040403	Sequence	427	32	2.9	30	6	AR077134	Sequence
355	18	AX063576	Sequence	32	2.9	18	6	AX063576	Sequence	428	32	2.9	30	6	AR087144	Sequence
356	18	AX081353	Sequence	32	2.9	18	6	AX081353	Sequence	429	32	2.9	30	6	AR087561	Sequence
357	18	AX083693	Sequence	32	2.9	18	6	AX083693	Sequence	430	32	2.9	30	6	AX180867	Sequence
358	18	AX088930	Sequence	32	2.9	18	6	AX088930	Sequence	431	32	2.9	30	6	AX468215	Sequence
359	18	AX103809	Sequence	32	2.9	18	6	AX103809	Sequence	432	32	2.9	30	6	E55287	Novel metal
360	18	AX103862	Sequence	32	2.9	18	6	AX103862	Sequence	433	32	2.9	30	6	E64508	Sugar-respo
361	18	AX103863	Sequence	32	2.9	18	6	AX103863	Sequence	434	32	2.9	30	6	I23958	Sequence 6
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363	18	AX105211	Sequence	32	2.9	18	6	AX105211	Sequence	436	32	2.9	31	6	AX248033	Sequence
364	18	AX278114	Sequence	32	2.9	18	6	AX278114	Sequence	437	32	2.9	31	6	AX248352	Sequence
365	18	AX283183	Sequence	32	2.9	18	6	AX283183	Sequence	438	32	2.9	31	6	AX248814	Sequence
366	18	AX283250	Sequence	32	2.9	18	6	AX283250	Sequence	439	32	2.9	31	6	BD005987	Galleatin
367	18	AX355727	Sequence	32	2.9	18	6	AX355727	Sequence	440	32	2.9	31	6	E10701	Primer. 9/1
368	18	AX355728	Sequence	32	2.9	18	6	AX355728	Sequence	441	32	2.9	31	6	E16002	Sequence 5
369	18	AX455638	Sequence	32	2.9	18	6	AX455638	Sequence	442	32	2.9	32	6	AR162778	Sequence
370	18	AX468484	Sequence	32	2.9	18	6	AX468484	Sequence	443	32	2.9	32	6	AR182223	Sequence
371	18	BD009103	Sequence	32	2.9	18	6	BD009103	Immunost	444	32	2.9	32	6	E06343	Primer. 9/1
372	18	I96098	Sequence 17	32	2.9	18	6	I96098	Sequence 17	445	32	2.9	32			

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 c 491 32 2.9 36 6 AX017162 Sequence
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 c 494 32 2.9 36 6 I92026 Sequence
 c 495 32 2.9 36 6 A31736 Sequence
 c 496 32 2.9 37 6 AR182877 Sequence
 c 497 32 2.9 37 6 AX424976 Sequence
 c 498 32 2.9 37 6 I20696 Sequence
 c 499 32 2.9 37 6 I20717 Sequence
 500 32 2.9 38 6 A23776 Sequence

ALIGNMENTS

RESULT 1
 AX377550/c
 LOCUS AX377550 39 bp DNA linear PAT 18-MAR-2002
 DEFINITION Sequence 27 from Patent WO0212553.
 ACCESSION AX377550
 VERSION AX377550.1 GI:19573736
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrendorf,H. and
 Muth,J.
 TITLE Method for detecting mutations in nucleotide sequences
 JOURNAL Patent: WO 0212553-A 27 14-FEB-2002;
 Nanogen Recognomics GmbH (DE)
 FEATURES Location/Qualifiers
 source 1..39
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 4 a 8 c 21 g 6 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.57e+03 Length: 39
 Score: 71.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.43% Indels: 0
 DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX377550 (1-39)

QY 53 ProGlyHisThrProHisProAlaSerArgAsp 64
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 39 CCCGGGCACAGCCGCCATCCAGCGCATCCCGCGAC 4

RESULT 2
 AX377551
 LOCUS AX377551 39 bp DNA linear PAT 18-MAR-2002
 DEFINITION Sequence 28 from Patent WO0212553.
 ACCESSION AX377551
 VERSION AX377551.1 GI:19573737
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrendorf,H. and
 Muth,J.
 TITLE Method for detecting mutations in nucleotide sequences
 JOURNAL Patent: WO 0212553-A 28 14-FEB-2002;
 Nanogen Recognomics GmbH (DE)
 FEATURES Location/Qualifiers
 source 1..39

Alignment Scores:
 Pred. No.: 1.57e+03 Length: 39
 Score: 71.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.43% Indels: 0
 DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX377551 (1-39)
 QY 53 ProGlyHisThrProHisProAlaSerArgAsp 64
 |||||
 39 CCCGGGCACAGCCGCCATCCAGCGCATCCCGCGAC 4

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 7 a 21 c 9 g 2 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.57e+03 Length: 39
 Score: 71.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.43% Indels: 0
 DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX377551 (1-39)

QY 53 ProGlyHisThrProHisProAlaSerArgAsp 64
 |||||
 3 CCCGGGCACAGCCGCCATCCAGCGCATCCCGCGAC 38

RESULT 3
 AR007301
 LOCUS AR007301 36 bp DNA linear PAT 04-DEC-1998
 DEFINITION Sequence 15 from patent US 5750390.
 ACCESSION AR007301
 VERSION AR007301.1 GI:3966785
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 36)
 AUTHORS Thompson,J.D. and Draper,K.G.
 TITLE Method and reagent for treatment of diseases caused by expression
 of the bcl-2 gene
 JOURNAL Patent: US 5750390-A 15 12-MAY-1998;
 FEATURES Location/Qualifiers
 source 1..36
 /organism="unknown"
 BASE COUNT 10 a 13 c 8 g 5 t
 ORIGIN

Alignment Scores:
 Pred. No.: 2.86e+03 Length: 36
 Score: 66.00 Matches: 11
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.98% Indels: 0
 DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR007301 (1-36)
 QY 181 LeuAsnArgHisLeuHisThrTriPleGlnAsp 191
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 3 CTGAACCGGACCTGCACACCTGGATCCAGGAT 35

RESULT 4
 AX377552
 LOCUS AX377552 39 bp DNA linear PAT 18-MAR-2002
 DEFINITION Sequence 29 from Patent WO0212553.
 ACCESSION AX377552
 VERSION AX377552.1 GI:19573738
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrendorf,H. and
 Muth,J.
 TITLE Method for detecting mutations in nucleotide sequences
 JOURNAL Patent: WO 0212553-A 29 14-FEB-2002;
 Nanogen Recognomics GmbH (DE)
 FEATURES Location/Qualifiers
 source 1..39

Alignment Scores:
 Pred. No.: 2.86e+03 Length: 36
 Score: 66.00 Matches: 11
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.98% Indels: 0
 DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR007301 (1-36)
 QY 181 LeuAsnArgHisLeuHisThrTriPleGlnAsp 191
 |||||
 3 CTGAACCGGACCTGCACACCTGGATCCAGGAT 35

RESULT 4
 AX377552
 LOCUS AX377552 39 bp DNA linear PAT 18-MAR-2002
 DEFINITION Sequence 29 from Patent WO0212553.
 ACCESSION AX377552
 VERSION AX377552.1 GI:19573738
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrendorf,H. and
 Muth,J.
 TITLE Method for detecting mutations in nucleotide sequences
 JOURNAL Patent: WO 0212553-A 29 14-FEB-2002;
 Nanogen Recognomics GmbH (DE)
 FEATURES Location/Qualifiers
 source 1..39

Alignment Scores:
 Pred. No.: 2.86e+03 Length: 36
 Score: 66.00 Matches: 11
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.98% Indels: 0
 DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR007301 (1-36)
 QY 181 LeuAsnArgHisLeuHisThrTriPleGlnAsp 191
 |||||
 3 CTGAACCGGACCTGCACACCTGGATCCAGGAT 35

RESULT 4
 AX377552
 LOCUS AX377552 39 bp DNA linear PAT 18-MAR-2002
 DEFINITION Sequence 29 from Patent WO0212553.
 ACCESSION AX377552
 VERSION AX377552.1 GI:19573738
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrendorf,H. and
 Muth,J.
 TITLE Method for detecting mutations in nucleotide sequences
 JOURNAL Patent: WO 0212553-A 29 14-FEB-2002;
 Nanogen Recognomics GmbH (DE)
 FEATURES Location/Qualifiers
 source 1..39

Alignment Scores:
 Pred. No.: 2.86e+03 Length: 36
 Score: 66.00 Matches: 11
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.98% Indels: 0
 DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR007301 (1-36)
 QY 181 LeuAsnArgHisLeuHisThrTriPleGlnAsp 191
 |||||
 3 CTGAACCGGACCTGCACACCTGGATCCAGGAT 35

RESULT 4
 AX377552
 LOCUS AX377552 39 bp DNA linear PAT 18-MAR-2002
 DEFINITION Sequence 29 from Patent WO0212553.
 ACCESSION AX377552
 VERSION AX377552.1 GI:19573738
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrendorf,H. and
 Muth,J.
 TITLE Method for detecting mutations in nucleotide sequences
 JOURNAL Patent: WO 0212553-A 29 14-FEB-2002;
 Nanogen Recognomics GmbH (DE)
 FEATURES Location/Qualifiers
 source 1..39

/organism="Homo sapiens"
 .db_xref="taxon:9606"
 7 a 20 c 9 g 3 t
 BASE COUNT
 ORIGIN

Alignment Scores:
 4.61e+03 Length: 39
 63.00 Matches: 11
 91.67% Conservativeness: 0
 91.67% Mismatches: 1
 5.71% Indels: 0
 6 Gaps: 0
 DB:

US-09-375-514-22 (1-205) x AX377552 (1-39)
 QY 53 ProGlyHisThrProHisProAlaSerArgAsp 64
 3 CCGGGCACACGCCCATTCAGCGGCATCCGGGCAC 38
 RESULT 5
 LOCUS AR007291
 DEFINITION Sequence 5 from patent US 5750390.
 ACCESSION AR007291
 VERSION AR007291.1 GI:3966775
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Thompson, J.D. and Draper, K.G.
 TITLE Method and reagent for treatment of diseases caused by expression
 of the bcl-2 gene
 JOURNAL Patent: US 5750390-A 5 12-MAY-1998;
 FEATURES Location/Qualifiers
 source 1..33
 /organism="unknown"
 5 a 16 c 7 g 5 t
 BASE COUNT
 ORIGIN

Alignment Scores:
 8.84e+03 Length: 33
 57.00 Matches: 10
 100.00% Conservativeness: 0
 100.00% Mismatches: 0
 5.16% Indels: 0
 6 Gaps: 0
 DB:

US-09-375-514-22 (1-205) x AR007291 (1-33)
 QY 46 ProGlyIlePheSerSerGlnProGlyHis 55
 Ddb 3 CCGGGCATCTTCTCTCCAGCGCGGCAC 32
 RESULT 6
 LOCUS AR007082/c
 DEFINITION Sequence 8 from patent US 5789201.
 ACCESSION AR007082
 VERSION AR007082.1 GI:3975397
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Guastella, J.
 TITLE Genes coding for bcl-2 homologues
 JOURNAL Patent: US 5789201-A 8 04-AUG-1998;
 FEATURES Location/Qualifiers
 source 1..24
 /organism="unknown"
 3 a 9 c 1 g 5 t 6 others
 BASE COUNT
 ORIGIN

Alignment Scores:
 24 bp DNA linear
 PAT 05-DEC-1998

X

Best Local Similarity: 100.00%
Query Match: 4.26%
DB: 6
Mismatches: 0
Indels: 0
Gaps: 0

US-09-375-514-22 (1-205) x I96085 (1-33)

QY 193 GlyGlyTrpValGlyAlaSerGly 200
Db 10 GGAGGCTGGGTAGGTGCATCTGCT 33

RESULT 9
AR007294

LOCUS AR007294 28 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 8 from patent US 5750390.

ACCESSION AR007294
VERSION AR007294.1 GI:3966778

KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 28)
AUTHORS Thompson,J.D. and Draper,K.G.

TITLE Method and reagent for treatment of diseases caused by expression of the bel-2 gene

JOURNAL Patent: US 5750390-A 8 12-MAY-1998;
FEATURES Location/Qualifiers

1..28
/organism="unknown"

BASE COUNT 3 a 13 c 7 g 5 t
ORIGIN

Alignment Scores:
Pred. No.: 3.81e+04

Score: 45.00 Length: 28
Percent Similarity: 100.00% Matches: 9
Best Local Similarity: 100.00% Conservative: 0

Query Match: 4.08% Mismatches: 0
DB: 6 Indels: 0 Gaps: 0

US-09-375-514-22 (1-205) x AR007294 (1-28)

QY 91 ProValValHisLeuAlaLeuArgGln 99

Db 1 CCTGTGGTCCACCTGGCCCTCCGCCAA 27

RESULT 10
HSAJ5138/c

LOCUS HSAJ5138 36 bp DNA linear PRI 27-AUG-1998
DEFINITION Homo sapiens CBS gene, intron 7, 5' end.

ACCESSION AJ005138

VERSION AJ005138.1 GI:3451235

KEYWORDS CBS gene; cystathionine beta-synthase.
SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 36)
AUTHORS Gaustadnes,M.

TITLE Direct Submission

JOURNAL Submitted (21-APR-1998) Gaustadnes M., Department of Clinical Biochemistry, Skejby University Hospital, Brendstrupgaardsvej, 8200 Aarhus N, DENMARK

REFERENCE 2 (bases 1 to 36)
AUTHORS Kraus,J.P., Le,K., Swaroop,M., Ohura,T., Tahara,T., Rosenberg,L.E., Roper,M.D. and Kozich,V.

TITLE Human cystathionine beta-synthase cDNA: sequence, alternative splicing and expression in cultured cells

JOURNAL Hum. Mol. Genet. 2 (10), 1633-1638 (1993)
MEDLINE 94093551
PUBMED 7903580

REFERENCE 3 (bases 1 to 36)
AUTHORS Gaustadnes,M., Kluijtmans,L.A., Jensen,O.K., Rasmussen,K., Heil,S.G., Kraus,J.P., Blom,H.J., Ingerslev,J. and Rudiger,N.

TITLE Detection of a novel deletion in the cystathionine beta-synthase (CBS) gene using an improved genomic DNA based method
JOURNAL FEBS Lett. 431 (2), 175-179 (1998)
MEDLINE 98372628
PUBMED 9708897

FEATURES source

Location/Qualifiers
1..36
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/map="q22.3"

gene 1..36

exon <1..6

intron /gene="CBS"
/number=7
7..>36

BASE COUNT 4 a 6 c 21 g 5 t
ORIGIN

Alignment Scores:
Pred. No.: 4.8e+04

Score: 45.00 Length: 36
Percent Similarity: 88.89% Matches: 7
Best Local Similarity: 77.78% Conservative: 1

Query Match: 4.08% Mismatches: 1
DB: 9 Indels: 0 Gaps: 0

US-09-375-514-22 (1-205) x HSAJ5138 (1-36)

QY 52 GlnProGlyHisThrProHisProAla 60

Db 27 CGGCGCGCCACACCACTCACCTGTGCA 1

RESULT 11
AR053546/c

LOCUS AR053546 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5834248.

ACCESSION AR053546

VERSION AR053546.1 GI:5978408

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Falb,D.

TITLE Compositions and methods using rchd534, a gene upregulated by shear stress

JOURNAL Patent: US 5834248-A 11 10-NOV-1998;
FEATURES Location/Qualifiers

1..24
source /organism="unknown"

BASE COUNT 4 a 14 c 1 g 5 t
ORIGIN

Alignment Scores:
Pred. No.: 3.77e+04

Score: 44.00 Length: 24
Percent Similarity: 100.00% Matches: 7
Best Local Similarity: 100.00% Conservative: 0

Query Match: 3.99% Mismatches: 0
DB: 6 Indels: 0 Gaps: 0

US-09-375-514-22 (1-205) x AR053546 (1-24)

QY 140 AspGlyValAsnTrpGlyArg 146

Db 23 GATGGGTGAACCTGGGGGAGG 3

RESULT 12
AR065873/c

LOCUS AR065873 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5849578.
ACCESSION AR065873
VERSION AR065873.1 GI:5996089
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Falb,D.A.
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular disease using rchd528 as a target
JOURNAL Patent: US 5849578-A 11 15-DEC-1998;
FEATURES Location/Qualifiers
source 1..24
BASE COUNT 4 a 14 c 1 g 5 t
ORIGIN
Alignment Scores: Length: 24
Pred. No.: 3.77e+04
Score: 44.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 3.99%
DB: 6
US-09-375-514-22 (1-205) x AR065873 (1-24)
QY 140 AspGlyValAsnTrpGlyArg 146
Db 23 GATGGGTGAACCTGGGGAGG 3
RESULT 13
AR080355/c AR080355 24 bp DNA linear PAT 31-AUG-2000
LOCUS AR080355
DEFINITION Sequence 11 from patent US 5968770.
ACCESSION AR080355
VERSION AR080355.1 GI:10007090
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Falb,D.A. and Gimbrone,M.A. Jr.
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular disease using rchd523 as a target
JOURNAL Patent: US 5968770-A 11 19-OCT-1999;
FEATURES Location/Qualifiers
source 1..24
BASE COUNT 4 a 14 c 1 g 5 t
ORIGIN
Alignment Scores: Length: 24
Pred. No.: 3.77e+04
Score: 44.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 3.99%
DB: 6
US-09-375-514-22 (1-205) x AR080355 (1-24)
QY 140 AspGlyValAsnTrpGlyArg 146
Db 23 GATGGGTGAACCTGGGGAGG 3
RESULT 14
AR148310/c AR148310 24 bp DNA linear PAT 08-AUG-2001
LOCUS AR148310
DEFINITION Sequence 11 from patent US 6225084.
ACCESSION AR148310

VERSION AR148310.1 GI:15112400
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Falb,D.A. and Gimbrone,M.A. Jr.
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular disease using rchd534 as a target
JOURNAL Patent: US 6225084-A 11 01-MAY-2001;
FEATURES Location/Qualifiers
source 1..24
BASE COUNT 4 a 14 c 1 g 5 t
ORIGIN
Alignment Scores: Length: 24
Pred. No.: 3.77e+04
Score: 44.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 3.99%
DB: 6
US-09-375-514-22 (1-205) x AR148310 (1-24)
QY 140 AspGlyValAsnTrpGlyArg 146
Db 23 GATGGGTGAACCTGGGGAGG 3
RESULT 15
AX031294 AX031294 28 bp DNA linear PAT 20-SEP-2000
LOCUS AX031294
DEFINITION Sequence 16 from Patent WO9914321.
ACCESSION AX031294
VERSION AX031294.1 GI:10278622
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 28)
AUTHORS O'Reilly,L., Puthalakath,H., Adams,J., O'Connor,L., Cory,S., Huang,D.C. and Strasser,A.
TITLE Novel therapeutic molecules
JOURNAL Patent: WO 9914321-A 16 25-MAR-1999;
INST MEDICAL W & E HALL (AU); PUTHALAKATH HAMSA (AU); REILLY LORRAINE O (AU); ADAMS JERRY (AU); CONNOR LIAM O (AU); CORY SUZANNE (AU); HUANG DAVID C S (AU); STRASSER ANDREAS (AU)
FEATURES Location/Qualifiers
source 1..28
BASE COUNT 8 a 11 c 6 g 3 t
ORIGIN
Alignment Scores: Length: 28
Pred. No.: 4.95e+04
Score: 43.00
Percent Similarity: 88.89%
Best Local Similarity: 88.89%
Query Match: 3.89%
DB: 6
US-09-375-514-22 (1-205) x AX031294 (1-28)
QY 184 HisLeuHisThrTrpIleGlnAspAsn 192
Db 1 CACCTGCACACCGCATCCAGGATAAC 27
RESULT 16
AX031320 AX031320 28 bp DNA linear UNA 20-SEP-2000
LOCUS AX031320
DEFINITION Sequence 16 from Patent WO9914321.

ACCESSION AX031320
VERSION AX031320.1 GI:10278645
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 28)
AUTHORS O'Reilly,L., Puthalakath,H., Adams,J., O'Connor,L., Cory,S.,
Huang,D.C. and Strasser,A.
TITLE Novel therapeutic molecules
JOURNAL Patent: WO 9914321-A 25-MAR-1999;
INST MEDICAL W & E HALL (AU) ; PUTHALAKATH HAMSA (AU) ; REILLY
LORRAINE O (AU) ; ADAMS JERRY (AU) ; CONNOR LIAM O (AU) ; CORY
SUZANNE (AU) ; HUANG DAVID C S (AU) ; STRASSER ANDREAS (AU)

FEATURES
source
1..28
/organism="unidentified"
/db_xref="taxon:32644" 3 t

BASE COUNT 8 a 11 c 6 g 3 t
ORIGIN

Alignment Scores:
Pred. No.: 4.95e+04 Length: 28
Score: 43.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 3.89% Indels: 0
DB: 13 Gaps: 0

US-09-375-514-22 (1-205) x AX031320 (1-28)

QY 184 HistLeuHsHrTpIleGlnAspAsn 192
Db 1 CACCTGCACACCGCGATCCAGGATAC 27

RESULT 17
AR090476/c
LOCUS AR090476 25 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 596 from patent US 5994076.
ACCESSION AR090476
VERSION AR090476.1 GI:10017231
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 25)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 596 30-NOV-1999;
FEATURES
source
1..25
/organism="unknown"

BASE COUNT 5 a 11 c 4 g 5 t
ORIGIN

Alignment Scores:
Pred. No.: 5.09e+04 Length: 25
Score: 42.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 3.80% Indels: 0
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR090476 (1-25)

QY 189 IleGlnAspAsnGlyGlyTrpVal 196
Db 24 ATCCAAGACCGGTTGGTGGTG 1

RESULT 18
AR197511/c
LOCUS AR197511 31 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 596 from patent US 6352829.

ACCESSION AR197511
VERSION AR197511.1 GI:20247360
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 25)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 596 05-MAR-2002;
FEATURES
source
1..25
/organism="unknown"

BASE COUNT 5 a 11 c 4 g 5 t
ORIGIN

Alignment Scores:
Pred. No.: 5.09e+04 Length: 25
Score: 42.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 3.80% Indels: 0
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR197511 (1-25)

QY 189 IleGlnAspAsnGlyGlyTrpVal 196
Db 24 ATCCAAGACCGGTTGGTGGTG 1

RESULT 19
I60569
LOCUS I60569 39 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 21 from patent US 5656725.
ACCESSION I60569
VERSION I60569.1 GI:2479014
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 39)
AUTHORS Chittenden,T.D. and Lutz,R.J.
TITLE Peptides and compositions which modulate apoptosis
JOURNAL Patent: US 5656725-A 21 12-AUG-1997;
FEATURES
source
1..39
/organism="unknown"

BASE COUNT 11 a 11 c 11 g 6 t
ORIGIN

Alignment Scores:
Pred. No.: 7.72e+04 Length: 39
Score: 42.00 Matches: 7
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 58.33% Mismatches: 3
Query Match: 3.80% Indels: 0
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x I60569 (1-39)

QY 101 GlyAspAspPheSerArgArgTyrArgGlyAspPhe 112
Db 1 GGGGACGACATCATCCAGCGTATGACTCAGAGTTC 36

RESULT 20
AX022526/c
LOCUS AX022526 31 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 3 from Patent EP0932674.
ACCESSION AX022526
VERSION AX022526.1 GI:10046124
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

unclassified.
 1 (bases 1 to 31)
 Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
 A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
 apoptosis-controlling genes
 JOURNAL Patent: EP 0932674-A 3 04-AUG-1999;
 AMRAD OPERATIONS PTY LTD (AU)
 FEATURES Location/Qualifiers
 source 1..31
 /organism="unidentified"
 /db_xref="taxon:32644"
 14
 /note="INOSINE (I)"
 17
 /note="INOSINE (I)"
 20
 /note="INOSINE (I)"
 5 a 10 c 5 g 7 t 4 others

BASE COUNT 5 a 10 c 5 g 7 t 4 others
 ORIGIN

Alignment Scores:
 Pred. No.: 7.12e+04 Length: 31
 Score: 41.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 3.71% Indels: 0
 DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX022526 (1-31)

QY 188 TrpIleGlnAspAsnGlyGlyTrp 195
 |||||
 Db 31 TGGATCCAGANMANGNGGCTGG 8

RESULT 21
 AX030814/c
 LOCUS 31 bp DNA linear PAT 20-SEP-2000
 DEFINITION Sequence 3 from Patent WO9735971.
 ACCESSION AX030814
 VERSION AX030814.1 GI:10278310
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 31)
 Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
 A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
 apoptosis-controlling genes
 JOURNAL Patent: WO 9735971-A 3 02-OCT-1997;
 ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU)
 ; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)
 FEATURES Location/Qualifiers
 source 1..31
 /organism="unidentified"
 /db_xref="taxon:32644"
 14
 /mod_base-i
 17
 /mod_base-i
 20
 /mod_base-i
 5 a 10 c 5 g 7 t 4 others

BASE COUNT 5 a 10 c 5 g 7 t 4 others
 ORIGIN

Alignment Scores:
 Pred. No.: 7.12e+04 Length: 31
 Score: 41.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 3.71% Indels: 0
 DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX030814 (1-31)

QY 188 TrpIleGlnAspAsnGlyGlyTrp 195
 |||||
 Db 31 TGGATCCAGANMANGNGGCTGG 8

RESULT 22
 I89980
 LOCUS 33 bp DNA linear PAT 10-AUG-1998
 DEFINITION Sequence 28 from patent US 5723318.
 ACCESSION I89980
 VERSION I89980.1 GI:3409920
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 33)
 Yamauchi,N., Kojima,T., Oh-eda,M. and Hattori,K.
 DNA coding for megakaryocyte potentiator
 JOURNAL Patent: US 5723318-A 28 03-MAR-1998;
 FEATURES Location/Qualifiers
 source 1..33
 /organism="unknown"
 1 a 13 c 14 g 5 t

BASE COUNT 1 a 13 c 14 g 5 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 7.55e+04 Length: 33
 Score: 41.00 Matches: 8
 Percent Similarity: 80.00% Conservative: 0
 Best Local Similarity: 80.00% Mismatches: 2
 Query Match: 3.71% Indels: 0
 DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x I89980 (1-33)

QY 76 AlaAlaProGlyAlaAlaAlaGlyProAla 85
 |||||
 Db 3 GCGGGCGCTGGTGGCCGCTGGGCCAGCC 32

RESULT 23
 S80834/c
 LOCUS 33 bp DNA linear PRI 07-MAY-1993
 DEFINITION gamma delta T cell antigen receptor delta-chain [V delta 2-J delta
 1 junction] [human, skin lesion, Genomic, 33 nt].
 ACCESSION S80834
 VERSION S80834.1 GI:245000
 KEYWORDS
 SOURCE Homo sapiens skin lesion.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Uyemura,K., Klotz,J., Pirmez,C., Ohmen,J., Wang,X.H., Ho,C.,
 Hoffman,W.L. and Modlin,R.L.
 TITLE Microanatomic clonality of gamma delta T cells in human
 JOURNAL leishmaniasis lesions
 MEDLINE J. Immunol. 148 (4), 1205-1211 (1992)
 PUBMED 92148143
 1531352
 REMARK GenBank staff at the National Library of Medicine created this
 entry [NCBI gibbsq 80834] from the original journal article.
 This sequence comes from Figure 4.

FEATURES Location/Qualifiers
 source 1..33
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

gene 1..33
 /partial

BASE COUNT 10 a 7 c 10 g 6 t
 ORIGIN /gene="gamma delta T cell antigen receptor delta-chain"

Alignment Scores:

Pred. No.: 7.55e+04 33
Score: 41.00 Length: 33
Matches: 7
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 3.71%
DB: 9 0
Gaps: 0

US-09-375-514-22 (1-205) x S80834 (1-33)

Qy 88 ProValProProValValHis 94

Db 21 OCTGTACCCCGAGTAGTTCAC 1
|||||

RESULT 24

LOCUS 165770/c 36 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 6 from patent US 5668294.

ACCESSION I65770

VERSION I65770.1 GI:2482340

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 36)

AUTHORS Meagher, R.B. and Summers, A.O.

TITLE Metal resistance sequences and transgenic plants

JOURNAL Patent: US 5668294-A 6 16-SEP-1997;

FEATURES Location/Qualifiers

source 1..36

BASE COUNT 8 a 13 c 9 g 6 t

ORIGIN

Alignment Scores:
Pred. No.: 8.19e+04 36
Score: 41.00 Length: 36
Matches: 8
Percent Similarity: 88.89%
Conservative: 0
Best Local Similarity: 88.89%
Mismatch: 1
Query Match: 3.71%
DB: 6 0
Indels: 0
Gaps: 0

US-09-375-514-22 (1-205) x I65770 (1-36)

Qy 75 ProAlaProGlyAlaAlaAGly 83

Db 35 CCTGCTGGCGGGTGGCTGCAGGA 9
|||||

RESULT 25

LOCUS AR168776/c 38 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 2 from patent US 6288042.

ACCESSION AR168776

VERSION AR168776.1 GI:17904871

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 38)

AUTHORS Rando, R.F., Ojwang, J.O., Hogan, M.E., Wallace, T.L. and Cossun, P.A.

TITLE Anti-viral guanidine-rich tetrad forming oligonucleotides

JOURNAL Patent: US 6288042-A 2 11-SEP-2001;

FEATURES Location/Qualifiers

source 1..38

BASE COUNT 0 a 0 c 29 g 9 t

ORIGIN

Alignment Scores:
Pred. No.: 8.61e+04 38
Score: 41.00 Length: 38
Matches: 8
Percent Similarity: 50.00%
Conservative: 0
Best Local Similarity: 50.00%
Mismatch: 2
Query Match: 3.71%
DB: 6 0
Indels: 2
Gaps: 6

DB: 6 Gaps: 1
US-09-375-514-22 (1-205) x AR168776 (1-38)

Qy 44 ProAlaProGlyIlePheSerGlnProGlyHisThrProHisPro 59

Db 32 CCCACCCCA-----CCCCCCCCACACCCACACCC 3
|||||

RESULT 26

LOCUS AR200245/c 38 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 2 from patent US 6355785.

ACCESSION AR200245

VERSION AR200245.1 GI:20250319

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 38)

AUTHORS Rando, R.F., Fennelwald, S., Zendeigui, J.G., Ojwang, J.O., Hogan, M.E.,

Pommier, Y., and Mazumder, A.

TITLE Guanidine-rich oligonucleotide integrase inhibitors

JOURNAL Patent: US 6355785-A 2 12-MAR-2002;

FEATURES Location/Qualifiers

source 1..38

BASE COUNT 0 a 0 c 29 g 9 t

ORIGIN

Alignment Scores:
Pred. No.: 8.61e+04 38
Score: 41.00 Length: 38
Matches: 8
Percent Similarity: 50.00%
Conservative: 0
Best Local Similarity: 50.00%
Mismatch: 2
Query Match: 3.71%
DB: 6 1
Indels: 6
Gaps: 1

US-09-375-514-22 (1-205) x AR200245 (1-38)

Qy 44 ProAlaProGlyIlePheSerGlnProGlyHisThrProHisPro 59

Db 32 CCCACCCCA-----CCCCCCCCACACCCACACCC 3
|||||

RESULT 27

LOCUS I27770/c 38 bp DNA linear PAT 06-FEB-1997

DEFINITION Sequence 2 from patent US 5567604.

ACCESSION I27770

VERSION I27770.1 GI:1818546

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 38)

AUTHORS Rando, R.F., Fennelwald, S., Zendeigui, J.G. and Ojwang, J.O.

TITLE Anti-viral guanidine-rich oligonucleotides

JOURNAL Patent: US 5567604-A 2 22-OCT-1996;

FEATURES Location/Qualifiers

source 1..38

BASE COUNT 0 a 0 c 29 g 9 t

ORIGIN

Alignment Scores:
Pred. No.: 8.61e+04 38
Score: 41.00 Length: 38
Matches: 8
Percent Similarity: 50.00%
Conservative: 0
Best Local Similarity: 50.00%
Mismatch: 2
Query Match: 3.71%
DB: 6 1
Indels: 6
Gaps: 1

US-09-375-514-22 (1-205) x I27770 (1-38)

QY 44 ProAlaProGlyIlePheSerSerGlnProGlyHisThrProHisPro 59
Db 32 CCCACCCA-----CCCCCCCCACACCCACACCC 3

RESULT 28
A47631
LOCUS A47631 35 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 8 from Patent EP0699755.
ACCESSION A47631
VERSION A47631.1 GI:2301576

KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 35)
Rodriguez,R.P., Valladares,J.L. and Mateo,D.A.
AUTHORS Method for obtaining modified immunoglobulins with reduced
TITLE immunogenicity of murine antibody variable domains, compositions
containing them

JOURNAL Patent: EP 0699755-A 8 06-MAR-1996;
IMMUNOLOGIA MOLECULAR CENTRO (CU)
COMMENT Other publication CA 2153135 951231.
FEATURES Location/Qualifiers

source
1..35
/organism="unidentified"
BASE COUNT 6 a 14 c 8 g 7 t
ORIGIN /db_xref="taxon:32644"

Alignment Scores:
Pred. No.: 9.11e+04 Length: 35
Score: 40.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 3.62% Indels: 0
DB: Gaps: 0

US-09-375-514-22 (1-205) x A47631 (1-35)

QY 45 AlaProGlyIlePheSerSerGlnProGly 54
Db 4 GCCCAGGCTTCTTCACTTCAGCCCGAGGC 33

RESULT 29
182275
LOCUS 182275 35 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 8 from patent US 5712120.
ACCESSION 182275
VERSION 182275.1 GI:3210572

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 35)
Rodriguez,R.Perez., Mateo de Acosta del Rio,C.Maria. and
AUTHORS Valladares,J.Lombardero.

TITLE Method for obtaining modified immunoglobulins with reduced
immunogenicity of murine antibody variable domains, compositions
containing them

JOURNAL Patent: US 5712120-A 8 27-JAN-1998;
FEATURES Location/Qualifiers

source
1..35
/organism="unknown"
BASE COUNT 6 a 14 c 8 g 7 t
ORIGIN

Alignment Scores:
Pred. No.: 9.11e+04 Length: 35
Score: 40.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 3.62% Indels: 0
DB: Gaps: 0

US-09-375-514-22 (1-205) x I82275 (1-35)

QY 45 AlaProGlyIlePheSerSerGlnProGly 54
Db 4 GCCCAGGCTTCTTCACTTCAGCCCGAGGC 33

RESULT 30
A47633/c
LOCUS A47633 36 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 10 from Patent EP0699755.
ACCESSION A47633

VERSION A47633.1 GI:2301578
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 36)
Rodriguez,R.P., Valladares,J.L. and Mateo,D.A.
AUTHORS Method for obtaining modified immunoglobulins with reduced
TITLE immunogenicity of murine antibody variable domains, compositions
containing them

JOURNAL Patent: EP 0699755-A 10 06-MAR-1996;
IMMUNOLOGIA MOLECULAR CENTRO (CU)
COMMENT Other publication CA 2153135 951231.
FEATURES Location/Qualifiers

source
1..36
/organism="unidentified"
BASE COUNT 8 a 8 c 14 g 6 t
ORIGIN /db_xref="taxon:32644"

Alignment Scores:
Pred. No.: 9.36e+04 Length: 36
Score: 40.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 3.62% Indels: 0
DB: Gaps: 0

US-09-375-514-22 (1-205) x A47633 (1-36)

QY 45 AlaProGlyIlePheSerSerGlnProGly 54
Db 32 GCCCAGGCTTCTTCACTTCAGCCCGAGGC 3

RESULT 31
A68670
LOCUS A68670 36 bp DNA linear PAT 06-MAY-1999
DEFINITION Sequence 16 from Patent WO9801550.
ACCESSION A68670

VERSION A68670.1 GI:4759684
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 36)
Cornelissen,A.W. and Schallig,H.D.
AUTHORS VACCINE AGAINST GASTRO-INTESTINAL NEMATODES
TITLE Patent: WO 9801550-A 16 15-JAN-1998;
JOURNAL UNIV UTRECHT (NL)

FEATURES Location/Qualifiers
source
1..36
/organism="unidentified"
BASE COUNT 10 a 4 c 15 g 7 t
ORIGIN /db_xref="taxon:32644"

Alignment Scores:
Pred. No.: 9.36e+04 Length: 36
Score: 40.00 Matches: 6
Percent Similarity: 85.71% Conservative: 0
Best Local Similarity: 85.71% Mismatches: 1
DB:

Query Match: 3.62% Indels: 0
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x A68670 (1-36)

Qy 27 GlyTyrGluTrpAspAlaGly 33
|||||
Db 10 GGATACGAATGGGATGAGGA 30

RESULT 32
182277/c
LOCUS 182277 36 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 10 from patent US 5712120.
ACCESSION I82277
VERSION I82277.1 GI:3210574
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 36)
Rodriguez,R.Perez., Mateo de Acosta del Rio,C.Maria. and
Valladares,J.Lombardero.
TITLE Method for obtaining modified immunoglobulins with reduced
immunogenicity of murine antibody variable domains, compositions
containing them
JOURNAL Patent: US 5712120-A 10 27-JAN-1998;
FEATURES Location/Qualifiers
source
1..36
/organism="unknown"
BASE COUNT 8 a 8 c 14 g 6 t
ORIGIN

Alignment Scores:
Pred. No.: 9.36e+04 Length: 36
Score: 40.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 3.62% Indels: 0
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x I82277 (1-36)

Qy 45 AlaProGlyIlePheSerSerGlnProGly 54
|||||
Db 32 GCCCAGGCTCTTCACCTTCAGCCCGCCAGC 3

RESULT 33
AR096669
LOCUS AR096669 40 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 7 from patent US 6008193.
ACCESSION AR096669
VERSION AR096669.1 GI:10025673
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 40)
Garfinkel,L. and Richter,T.
TITLE Methods of using human von Willebrand factor GPIb binding domain
polypeptides
JOURNAL Patent: US 6008193-A 7 28-DEC-1999;
FEATURES Location/Qualifiers
source
1..40
/organism="unknown"
BASE COUNT 11 a 14 c 8 g 7 t
ORIGIN

Alignment Scores:
Pred. No.: 1.03e+05 Length: 40
Score: 40.00 Matches: 6
Percent Similarity: 85.71% Conservative: 0
Best Local Similarity: 85.71% Mismatches: 1
Query Match: 3.62% Indels: 0

DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR096669 (1-40)

Qy 53 ProGlyHisThrProHisPro 59
|||||
Db 1 CCAGGACGAACGCCACATCCA 21

RESULT 34
AX262441/c
LOCUS AX262441 40 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 16 from Patent WO0172119.
ACCESSION AX262441
VERSION AX262441.1 GI:16511355
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Cornali,E., Nehls,M.C., Schlueter,V., Wattler,F., Wattler,S. and
Wolf,S.
TITLE Non-human animal model for growth deficiency and information
processing or cognitive function defects and use thereof
JOURNAL Patent: WO 0172119-A 16 04-OCT-2001;
Ingenium Pharmaceuticals AG (DE)
FEATURES Location/Qualifiers
source
1..40
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"
BASE COUNT 5 a 15 c 16 g 4 t
ORIGIN

Alignment Scores:
Pred. No.: 1.03e+05 Length: 40
Score: 40.00 Matches: 7
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 3.62% Indels: 0
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX262441 (1-40)

Qy 33 GlyAspValGlyAlaAlaProGly 41
|||||
Db 40 GGAGACTCGGAGCTGTGCTCCCGC 14

RESULT 35
AX248386
LOCUS AX248386 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 465 from Patent WO0166800.
ACCESSION AX248386
VERSION AX248386.1 GI:15863009
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 465 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES Location/Qualifiers
source
1..31
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 8 a 7 c 8 g 7 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 9.3e+04 Length: 31
Score: 39.00 Matches: 5

Percent Similarity: 77.78% Conservative: 2
Best Local Similarity: 55.56% Mismatches: 2
Query Match: 3.53% Indels: 0
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX248386 (1-31)

QY 28 TyrGlutPaspAlaGlyaspValGly 36

Db 1 TATGATTGGATCCCRAGGACATAGGC 27

RESULT 36

AX097404/c

LOCUS

DEFINITION

AX097404

ACCESSION

VERSION

AX097404.1

GI:13513964

KEYWORDS

synthetic construct.

ORGANISM

synthetic construct

artificial sequences.

REFERENCE

1 (bases 1 to 35)

AUTHORS

Kaplan, H., Entwistle, J., Tanha, J., Narang, S. and Dan, M.

TITLE

Enhanced phage display libraries of human vH fragments and methods

JOURNAL

Patent: WO 0118058-A 29 15-MAR-2001;

Novopharm Biotech, Inc. (CA)

FEATURES

Location/Qualifiers

1..35

source

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="primer"

BASE COUNT

10 a 9 c 12 g 4 t

ORIGIN

Alignment Scores:

Pred. No.: 1.04e+05

Score: 39.00

Matches: 6

Conservative: 1

Best Local Similarity: 70.00%

Mismatches: 3

Indels: 0

Query Match: 6

DB: 6

US-09-375-514-22 (1-205) x AX097404 (1-35)

QY 40 ProGlyAlaAlaProAlaProGlyIlePhe 49

Db 33 CCTGCAGCTGGACCTCGGCTGGTCTTC 4

RESULT 37

AR202261/c

LOCUS

DEFINITION

AX202261

ACCESSION

VERSION

AR202261.1

GI:20256800

KEYWORDS

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 40)

AUTHORS

Bauer, S. Christopher., Abrams, M. Allen., Braford-Goldberg, S. Ruth.,

Caparon, M. Helena., Easton, A. Michael., Klein, B. Kure., McKearn, J. P.,

Olins, P. O., Pak, K. and Thomas, J. W.

TITLE

Methods of using multivalent IL-3 hematopoiesis fusion protein

JOURNAL

Patent: US 6361577-A 110 26-MAR-2002;

FEATURES

Location/Qualifiers

1..40

source

/organism="unknown"

BASE COUNT

8 a 8 c 13 g 11 t

ORIGIN

Alignment Scores:

Pred. No.: 1.18e+05

Length: 40

Score: 39.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 3.53% Indels: 0
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR202261 (1-40)

QY 84 proAlaLeuSerProValProPro 91

Db 38 CCTGCCATGGCTCCAGTACCACCA 15

RESULT 38

AX080990/c

LOCUS

DEFINITION

AX080990

ACCESSION

VERSION

AX080990.1

GI:13169927

KEYWORDS

synthetic construct.

ORGANISM

synthetic construct

artificial sequences.

REFERENCE

1 (bases 1 to 40)

AUTHORS

Hermanson, G.G.

TITLE

Flt-3 ligand-encoding polynucleotide as a polynucleotide-based

JOURNAL

Patent: WO 0109303-A 40 08-FEB-2001;

VICAL INCORPORATED (US)

FEATURES

Location/Qualifiers

1..40

source

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="DNA Primer"

BASE COUNT

6 a 16 c 11 g 7 t

ORIGIN

Alignment Scores:

Pred. No.: 1.18e+05

Score: 39.00

Matches: 6

Conservative: 2

Best Local Similarity: 80.00%

Mismatches: 2

Indels: 0

Query Match: 6

DB: 6

US-09-375-514-22 (1-205) x AX080990 (1-40)

QY 138 PheArgAspGlyValAsnTrpGlyArgIle 147

Db 40 TGGGAGATGGATACAGTTGGGGCCGCATC 11

RESULT 39

AX248293

LOCUS

DEFINITION

AX248293

ACCESSION

VERSION

AX248293.1

GI:15862916

KEYWORDS

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 31)

AUTHORS

Cargill, M., Ireland, J. S. and Lander, E. S.

TITLE

Human single nucleotide polymorphisms

JOURNAL

Patent: WO 0166800-A 372 13-SEP-2001;

WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

FEATURES

Location/Qualifiers

1..31

source

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT

3 a 6 c 17 g 4 t

ORIGIN

1 others

JOURNAL Patent: WO 9910529-A 2 04-MAR-1999;
MORTEN JOHN EDWARD NORRIS (GB); ZENECA LTD (GB)

FEATURES
source
Location/Qualifiers
1..30
/organism="unidentified"
/db_xref="taxon:32644" 1 t

BASE COUNT 2 a 9 c 18 g 1 t
ORIGIN

Alignment Scores:
Pred. No.: 1.03e+05 Length: 30
Score: 38.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 3.44% Indels: 0
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x A98608 (1-30)

38 AlaProGlyAlaAlaProAla 45

Db 29 GCCCGCGCTGGAGCGCCCGCC 6

RESULT 44

S66556
LOCUS S66556 30 bp DNA linear PRI 05-MAY-2000
DEFINITION COL1A1-collagen alpha 1(I) chain (exon 43) [human, Genomic Mutant,
30 nt].

ACCESSION S66556
VERSION S66556.1 GI:239218

KEYWORDS
SOURCE

ORGANISM Homo sapiens;

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 30)

AUTHORS Hawkins,J.R., Superti-Furga,A., Steinmann,B. and Dalglish,R.

TITLE A 9-base pair deletion in COL1A1 in a lethal variant of

JOURNAL osteogenesis imperfecta

MEDLINE J. Biol. Chem. 266 (33), 22370-22374 (1991)

PUBMED 92042176

REMARK 1939261

GenBank staff at the National Library of Medicine created this

entry [NCBI gibbsq 66556] from the original journal article.

This sequence comes from Figure 3.

FEATURES

source

1..30

/organism="Homo sapiens"

/db_xref="taxon:9606"

<1..>30

/gene="COL1A1"

/note="collagen alpha 1(I) chain"

<1..>30

/gene="COL1A1"

/note="This sequence comes from Figure 3; 9 base pair

deletion; conceptual translation presented here differs

from translation in publication"

/codon_start=1

/product="collagen alpha 1(I) chain"

/protein_id="AAB20361.1"

/db_xref="GI:239219"

/translation="GPPGAPGAPG"

1 a 13 c 10 g 6 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 1.03e+05 Length: 30

Score: 38.00 Matches: 7

Percent Similarity: 77.78% Conservative: 0

Best Local Similarity: 77.78% Mismatches: 2

Query Match: 3.44% Indels: 0

DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x S66556 (1-30)

QY 39 ProGlyAlaAlaProAlaProGly 47

Db 4 CCCCCTGGTCTCTCTGGTGGCCCTGGC 30

RESULT 45

AX248864/c 31 bp DNA linear PAT 28-SEP-2001

LOCUS AX248864

DEFINITION Sequence 943 from Patent WO0166800.

ACCESSION AX248864

VERSION AX248864.1 GI:15863487

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 31)

AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.

TITLE Human single nucleotide polymorphisms

JOURNAL Patent: WO 0166800-A 943 13-SEP-2001;

WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

FEATURES Location/Qualifiers

1..31

/organism="Homo sapiens"

/db_xref="taxon:9606"

5 a 10 c 13 g 2 t 1 others

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 1.06e+05 Length: 31

Score: 38.00 Matches: 6

Percent Similarity: 87.50% Conservative: 1

Best Local Similarity: 75.00% Mismatches: 1

Query Match: 3.44% Indels: 0

DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX248864 (1-31)

QY 40 ProGlyAlaAlaProAlaProGly 47

Db 31 CCAGGGTCGCTCCACCCCTGGG 8

RESULT 46

AX477731 31 bp DNA linear PAT 12-AUG-2002

LOCUS AX477731

DEFINITION Sequence 13 from Patent WO0240530.

ACCESSION AX477731

VERSION AX477731.1 GI:22216878

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1

AUTHORS Fesik,S.W., Petros,A.M., Yoon,H. and Nettlesheim,D.G.

TITLE Mutant bcl-2 proteins and uses thereof

JOURNAL Patent: WO 0240530-A 13 23-MAY-2002;

ABBOTT LABORATORIES (US)

FEATURES Location/Qualifiers

1..31

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="Primer" 9 g 4 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 1.06e+05 Length: 31

Score: 38.00 Matches: 8

Percent Similarity: 88.89% Conservative: 0

Best Local Similarity: 88.89% Mismatches: 1

Query Match: 3.44% Indels: 0

DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX477731 (1-31)

Qy 92 ValValHisLeuAlaLeuArgGlnAla 100
 Db 4 GTGTCACCTGACCTCCGCCAAGCC 30

RESULT 47
 AX477732/c

LOCUS AX477732 31 bp DNA linear PAT 12-AUG-2002

DEFINITION Sequence 14 from Patent WO0240530.

ACCESSION AX477732

VERSION AX477732.1 GI:22216879

KEYWORDS synthetic construct.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Fesik, S.W., Petros, A.M., Yoon, H. and Nettesheim, D.G.

TITLE Mutant bcl-2 proteins and uses thereof

JOURNAL Patent: WO 0240530-A 14 23-MAY-2002;

ABBOTT LABORATORIES (US)

FEATURES

source

1. .31

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="Primer"

Location/Qualifiers

4 a 9 c 13 g 5 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 1.06e+05

Score: 38.00

Matches: 8

Conservative: 0

Best Local Similarity: 88.89%

Mismatches: 1

Query Match: 3.44%

Indels: 0

Gaps: 0

DB:

US-09-375-514-22 (1-205) x AX477732 (1-31)

Qy 92 ValValHisLeuAlaLeuArgGlnAla 100

Db 28 GTGTCACCTGACCTCCGCCAAGCC 2

RESULT 48

A36722

LOCUS A36722 33 bp DNA linear PAT 05-MAR-1997

DEFINITION Sequence 10 from Patent EP0586112.

ACCESSION A36722

VERSION A36722.1 GI:2293991

KEYWORDS Hepatitis C virus.

SOURCE Hepatitis C virus.

ORGANISM Hepatitis C virus.

REFERENCE 1 (bases 1 to 33)

AUTHORS Tercero, J.C., Garcia, L.C., Ramos, J.A. and Alemany, J.C.

TITLE Control of PCR mediated detection of micro-organisms

JOURNAL Patent: EP 0586112-A 10 09-MAR-1994;

PHARMA GEN S A (ES)

COMMENT Other publication JP 7087978 950404.

FEATURES

source

1. .33

/organism="Hepatitis C virus"

/db_xref="taxon:11103"

8 a 11 c 8 g 6 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 1.13e+05

Score: 38.00

Matches: 8

Conservative: 1

Best Local Similarity: 80.00%

Mismatches: 1

Query Match:

Length: 33

Matches: 8

Conservative: 1

Mismatches: 1

Indels: 0

Gaps: 0

DB:

US-09-375-514-22 (1-205) x AX477732 (1-31)

Qy 83 GlyProAlaLeuSerProValPro 90

Db 36 GGTCCCGCACATACCCCGGTACCC 13

RESULT 50

AR052605/c

LOCUS AR052605 20 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 3 from patent US 5831066.

ACCESSION AR052605

VERSION AR052605.1 GI:5975969

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 20)

AUTHORS Read, J.C.

TITLE Regulation of bcl-2 gene expression

JOURNAL Patent: US 5831066-A 3 03-NOV-1998;

FEATURES

source

1. .20

/organism="unknown"

4 a 10 c 3 g 3 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 8.06e+04

Score: 37.00

Matches: 6

Conservative: 0

Best Local Similarity: 100.00%

Mismatches: 0

Query Match:

Length: 20

Matches: 6

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

DB:

US-09-375-514-22 (1-205) x A36722 (1-33)

Qy 60 AlaAlaSerArgAspProValAlaArgThr 69

Db 2 GCAGCTCCAGGATTCACCAATTGCCAGGACG 31

RESULT 49

AX247606/c

LOCUS AX247606 38 bp DNA linear PAT 28-SEP-2001

DEFINITION Sequence 27 from Patent WO0166804.

ACCESSION AX247606

VERSION AX247606.1 GI:15862295

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 38)

AUTHORS Cronin, M.T., Frueh, F. and Brennan, T.M.

TITLE Methods for optimizing hybridization performance of polynucleotide

JOURNAL probes and localizing and detecting sequence variations

Patent: WO 0166804-A 27 13-SEP-2001;

Proteome Laboratories, Inc. (US)

FEATURES

source

1. .38

/organism="Homo sapiens"

/db_xref="taxon:9606"

8 a 7 c 16 g 7 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 1.28e+05

Score: 38.00

Matches: 7

Conservative: 0

Best Local Similarity: 87.50%

Mismatches: 1

Query Match: 3.44%

Indels: 0

Gaps: 0

DB:

DB: 6 Gaps: 0
US-09-375-514-22 (1-205) x AR052605 (1-20)
QY 193 GlyGlyTrpValcIyAia 198
Db 20 GGAGGCTGGTAGGTGCA 3

Search completed: May 31, 2003, 22:59:21
Job time : 1776 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 31, 2003, 17:00:06 ; Search time 215 Seconds
(without alignments)
2147.254 Million cell updates/sec

Title: US-09-375-514-22

Perfect score: 1104

Sequence: 1 MAHAGRTGYDREIVMKYIH.....HTWIQDNGGWWGASGDVSLG 205

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2056596

Minimum DB seq length: 10
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q/cq2_1/USPto_spool/US09375514/runat_28052003_165345_18650/app_query.fasta_1.391
-DB=N_Geneseq_101002 -QMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MAYRIX=blom62 -TRANS=human40.cdi
-LIST=500 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=50
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=10 -MAXLEN=40
-USER=US09375514.@CN_1.1.208.@runat_28052003_165345_18650 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	6.0	36	14	BCL-2 mRNA ribozym
2	57	5.2	33	14	BCL-2 mRNA ribozym
3	55	5.0	24	19	Rat bcl-2 downstre
4	55	5.0	24	20	PCR primer used to
5	50	4.5	33	22	Human proteolytic
6	50	4.5	36	22	Human Bcl-2 PCR pr
7	49	4.4	24	24	Bcl-2 related olig
8	49	4.4	24	24	Bcl-2 splice donor
9	47	4.3	33	16	Bcl-2 related olig
10	47	4.3	33	19	Human bcl-2 oligon
11	47	4.3	33	33	Bcl-2 antisense ol
12	45	4.1	28	14	BCL-2 mRNA ribozym
13	44	4.0	24	17	bcl-2 reverse PCR
14	44	4.0	24	20	Reverse primer for
15	44	4.0	24	20	Mouse bcl-2 revers
16	44	4.0	24	20	PCR primer for mou
17	44	4.0	24	21	Reverse primer for
18	44	4.0	24	21	Mouse bcl-2 revers
19	44	4.0	25	21	Bcl-2 specific gen
20	44	4.0	27	22	Human Bcl-2 mutag
21	44	4.0	27	24	Human bcl-2 mRNA p
22	42	3.8	25	24	Human gene specifi
23	42	3.8	27	22	Human Bcl-2 mutag
24	42	3.8	27	22	Human Bcl-2 mutag
25	42	3.8	39	17	GD domain region f
26	42	3.8	39	24	DNA encoding Bak G
27	41	3.7	27	22	Human Bcl-2 mutag
28	41	3.7	27	22	Human Bcl-2 mutag
29	41	3.7	31	18	Mouse bcl-2 gene p
30	41	3.7	36	18	Mercuric ion reduc
31	41	3.7	36	20	Primer 3' N for Tn2
32	41	3.7	38	14	erb B2/neu promote
33	41	3.7	38	15	Steroid hormone re
34	41	3.7	38	15	Guanosine rich oli
35	41	3.7	38	18	Viral integrase in
36	41	3.7	38	19	Oligonucleotide #4
37	41	3.6	39	16	Cdn primer Bcl2 2-
38	40	3.6	24	24	Fluorescent probe
39	40	3.6	27	17	Cytokine productio
40	40	3.6	27	22	Human Bcl-2 mutag
41	40	3.6	40	12	vWF GPIb binding d
42	40	3.6	40	20	Human mature von W
43	40	3.6	40	20	Probe for Von Will
44	40	3.6	40	21	A. fumigatus codon
45	40	3.6	40	22	Murine growth horm
46	40	3.6	40	23	Bcl-2 antisense ol
47	39	3.5	23	21	Bcl-2 antisense ol
48	39	3.5	23	21	Human Bcl-2 mutag
49	39	3.5	27	22	Human Bcl-2 mutag
50	39	3.5	27	22	Human Bcl-2 mutag
51	39	3.5	32	20	Human Bcl-2 antise
52	39	3.5	32	20	C/EBP-beta antisen
53	39	3.5	32	21	Human C/EBP polynu
54	39	3.5	32	21	Human adenosine re
55	39	3.5	33	21	C/EBP-beta antisen
56	39	3.5	33	21	Human C/EBB polynu
57	39	3.5	33	21	Human adenosine re
58	39	3.5	34	20	C/EBP-beta antisen
59	39	3.5	34	21	Human C/EBB polynu
60	39	3.5	34	21	Human adenosine re
61	39	3.5	35	20	C/EBP-beta antisen
62	39	3.5	35	21	Human C/EBB polynu
63	39	3.5	35	21	Human adenosine re
64	39	3.5	35	22	VH ligand-binding
65	39	3.5	36	20	C/EBP-beta antisen
66	39	3.5	36	21	Human C/EBB polynu
67	39	3.5	36	21	Human adenosine re

68	39	3.5	37	20	AA54974	C/EBP-beta antisen	c 141	36	3.3	20	22	AA515195	Human bcl-x antise
69	39	3.5	37	21	AA54974	Human C/EBP polyu	c 142	36	3.3	20	22	AAH27691	Human bcl-x antise
70	39	3.5	37	21	AA54974	Human adenosine re	c 143	36	3.3	20	22	AB196903	Capture oligonucle
71	39	3.5	38	20	AA54973	C/EBP-beta antisen	c 144	36	3.3	23	14	AAO51950	BCL-2 mRNA ribozym
72	39	3.5	38	21	AA54973	Human C/EBP polyu	c 145	36	3.3	24	24	AB190376	Capture oligonucle
73	39	3.5	38	21	AA54973	Human adenosine re	c 146	36	3.3	24	24	AB190377	Capture oligonucle
c 74	39	3.5	39	13	AAQ20998	DNA probe pl-79.	c 147	36	3.3	25	24	AB199998	Left PCR primer us
75	39	3.5	39	20	AA54972	C/EBP-beta antisen	c 148	36	3.3	25	24	ABN04782	Human GDMPL-1 25-m
76	39	3.5	39	21	AA54972	Human C/EBP polyu	c 149	36	3.3	25	24	ABN04783	Human GDMPL-1 25-m
77	39	3.5	39	21	AA54972	Human adenosine re	c 150	36	3.3	25	24	ABN04784	Human GDMPL-1 25-m
78	39	3.5	40	16	AA54972	Oligonucleotide #H	c 151	36	3.3	25	24	ABN04785	Human GDMPL-1 25-m
79	39	3.5	40	20	AA54971	C/EBP-beta antisen	c 152	36	3.3	25	24	ABN04786	Human GDMPL-1 25-m
80	39	3.5	40	21	AA54971	Human C/EBP polyu	c 153	36	3.3	25	24	ABN04787	Human GDMPL-1 25-m
81	39	3.5	40	21	AA54971	Human adenosine re	c 154	36	3.3	25	24	ABN04788	Human GDMPL-1 25-m
c 82	39	3.5	40	22	AA54971	Mouse kappa light	c 155	36	3.3	25	24	ABN04789	Human GDMPL-1 25-m
83	38.5	3.5	31	22	AA129884	Human single nucle	c 156	36	3.3	27	24	ABK52426	Human FGF-related
84	38	3.4	20	22	AA129884	Human Bcl-2 protei	c 157	36	3.3	28	15	AAQ79214	Guanosine rich oli
85	38	3.4	20	22	AA129884	Human Bcl-2 protei	c 158	36	3.3	29	24	ABK49675	Mouse intron 1 3'
86	38	3.4	22	21	AA54972	BCL-2 RNA RT-PCR pr	c 159	36	3.3	30	16	AAQ99758	Primer #1 for ampl
87	38	3.4	24	21	AA54972	BCL-2 PCR primer #	c 160	36	3.3	30	21	AAQ99758	Multiplex analysis
88	38	3.4	24	22	AA54972	Human BCL-2 PCR pr	c 161	36	3.3	30	21	AA428653	PCR primer for mou
89	38	3.4	24	22	AA54972	Diagnostic primer	c 162	36	3.3	30	22	AA428653	Human haemochromat
c 90	38	3.4	30	20	AA54972	Human single nucle	c 163	36	3.3	30	23	AA515717	Haemochromatosis s
91	38	3.4	33	15	AA54972	Matagenic primer M	c 164	36	3.3	30	23	AA515717	Otoferlin exon/int
92	38	3.4	36	19	AA54972	Human bak BH2 doma	c 165	36	3.3	31	21	AAH78940	Human genomic DNA
93	38	3.4	37	24	AA54972	Penton-base adenov	c 166	36	3.3	31	21	AAH78940	Human single nucle
c 94	38	3.4	38	22	AA54972	Beta actin gene pr	c 167	36	3.3	32	17	AAH78940	5' primer for CD34
c 95	38	3.4	38	24	AA54972	Human wt1 truncati	c 168	36	3.3	32	18	AAH78940	Human G protein co
c 96	37	3.4	20	19	AA54972	Human bcl-2 antise	c 169	36	3.3	32	21	AAH78940	Human ECD-deltaPD
97	37	3.4	20	21	AA54972	PCR primer for hum	c 170	36	3.3	32	24	ABK52426	Human Her-2/neu EC
c 98	37	3.4	20	21	AA54972	Bcl-2 antisenase ol	c 171	36	3.3	32	10	AAH78940	Molecular stick DN
c 99	37	3.4	24	21	AA54972	Brevibacterium lac	c 172	36	3.3	35	22	AAH78940	Thrombin receptor
c 100	37	3.4	24	21	AA54972	Bcl-2 RNA-DNA hybr	c 173	36	3.3	36	13	AAQ28347	fdTetBSN vector ol
c 101	37	3.4	24	21	AA54972	First type III-C a	c 174	36	3.3	36	16	AAQ28347	DNA PCR primer RA0
c 102	37	3.4	28	14	AA54972	Fibronectin PCR 3'	c 175	36	3.3	37	18	AAH78940	Probe for bovine t
c 103	37	3.4	28	14	AA54972	Human fibronectin	c 176	36	3.3	38	12	AAQ28347	E-cadherin SNP pro
c 104	37	3.4	28	19	AA54972	Human C/EBP-beta antisen	c 177	36	3.3	38	13	AAQ28347	Reporter vector in
c 105	37	3.4	28	20	AA54972	Human C/EBP polyu	c 178	36	3.3	38	13	AAQ28347	IL-4 2'F/NH2 RNA 1
c 106	37	3.4	29	20	AA54972	Human adenosine re	c 179	36	3.3	38	14	AAQ28347	Primer JSS33(B) us
c 107	37	3.4	29	21	AA54972	C/EBP-beta antisen	c 180	36	3.3	38	14	AAQ28347	Human IL4Ralpha ge
c 108	37	3.4	29	21	AA54972	Human C/EBP polyu	c 181	36	3.3	39	21	AAH78940	Corn male reproduc
c 109	37	3.4	29	24	AA54972	Human adenosine re	c 182	36	3.3	39	22	AAH78940	Oligonucleotide fr
c 110	37	3.4	30	20	AA54972	Human C/EBP-beta antisen	c 183	36	3.3	39	22	AAH78940	Guanosine rich oli
c 111	37	3.4	30	21	AA54972	Human C/EBP polyu	c 184	36	3.3	39	22	AAH78940	Viral integrase in
c 112	37	3.4	31	21	AA54972	Human adenosine re	c 185	36	3.3	39	24	ABK27885	Oligonucleotide #1
c 113	37	3.4	31	21	AA54972	Human C/EBP polyu	c 186	36	3.3	39	24	ABK27885	Viral integrase in
c 114	37	3.4	31	21	AA54972	Human adenosine re	c 187	36	3.3	39	24	ABK27885	Oligonucleotide #1
c 115	37	3.4	31	21	AA54972	Human C/EBP polyu	c 188	36	3.3	39	24	ABK27885	Oligonucleotide #1
c 116	37	3.4	31	21	AA54972	Human single nucle	c 189	36	3.3	39	24	ABK27885	Synthetic oligonuc
c 117	37	3.4	31	22	AA54972	Human single nucle	c 190	36	3.3	39	24	ABK27885	Human protease act
c 118	37	3.4	32	18	AA54972	Spider silk protei	c 191	36	3.3	39	24	ABK27885	PAR PCR primer SEQ
c 119	37	3.4	33	22	AA54972	Human IL-17RH2 hyb	c 192	36	3.3	39	24	ABK27885	PCR primer DLX3E3F
c 120	37	3.4	34	22	AA54972	Chimeric RGS prote	c 193	36	3.3	39	24	ABK27885	Bcl-2 related olig
c 121	37	3.4	35	24	AA54972	Cricetulus griseus	c 194	36	3.3	39	24	ABK27885	SNP specific lower
c 122	37	3.4	35	14	AA54972	HIV4par, directed	c 195	36	3.3	39	24	ABK27885	Oligonucleotide SP
c 123	37	3.4	38	11	AA54972	Sequence binding t	c 196	36	3.3	39	24	ABK27885	Human zinc-finger
c 124	37	3.4	38	13	AA54972	Triplex forming ol	c 197	36	3.3	39	24	ABK27885	Oligonucleotide us
c 125	37	3.4	38	15	AA54972	Sequence of synth	c 198	36	3.3	39	24	ABK27885	Human GDMPL-1 25-m
c 126	37	3.4	38	15	AA54972	Sequence of contro	c 199	36	3.3	39	24	ABK27885	Human GDMPL-1 25-m
c 127	37	3.4	38	15	AA54972	Sequence of synth	c 200	36	3.3	39	24	ABK27885	Human GDMPL-1 25-m
c 128	37	3.4	38	15	AA54972	Triple helix-formi	c 201	36	3.3	39	24	ABK27885	Human GDMPL-1 25-m
c 129	37	3.4	38	15	AA54972	Triple helix-formi	c 202	36	3.3	39	24	ABK27885	Human GDMPL-1 25-m
c 130	37	3.4	38	15	AA54972	Guanosine rich oli	c 203	36	3.3	39	24	ABK27885	Human GDMPL-1 25-m
c 131	37	3.4	38	18	AA54972	Viral integrase in	c 204	36	3.3	39	24	ABK27885	Human GDMPL-1 25-m
c 132	37	3.4	38	18	AA54972	Oligonucleotide #3	c 205	36	3.3	39	24	ABK27885	Human GDMPL-1 25-m
c 133	37	3.4	40	17	AA54972	BCG deletion regio	c 206	36	3.3	39	24	ABK27885	Human GDMPL-1 25-m
c 134	37	3.4	40	20	AA54972	Circular plasmid e	c 207	36	3.3	39	24	ABK27885	Human GDMPL-1 25-m
c 135	37	3.4	40	21	AA54972	Polynucleotide seq	c 208	36	3.3	39	24	ABK27885	Human GDMPL-1 25-m
c 136	37	3.4	40	21	AA54972	Oligonucleotide 33	c 209	36	3.3	39	24	ABK27885	Human GDMPL-1 25-m
c 137	36	3.3	19	21	AA54972	Probe hybridising	c 210	36	3.3	39	24	ABK27885	VEGF 2'-NH2-RNA nu
c 138	36	3.3	20	20	AA54972	Synthetic RNA sequ	c 211	36	3.3	39	24	ABK27885	Genomic sequence s
c 139	36	3.3	20	20	AA54972	Antisense oligonuc	c 212	36	3.3	39	24	ABK27885	Oligonucleotide us
c 140	36	3.3	20	21	AA54972	Antisense oligonuc	c 213	36	3.3	39	24	ABK27885	Bcl-2 antisense ol

c 214	35	3.2	26	22	AA75967	Rat Bcl-XL mutagen	287	34	3.1	24	24	ABI86275
c 215	35	3.2	27	21	AAZ50048	5' PCR primer-2 fo	288	34	3.1	25	21	AAC95580
c 216	35	3.2	28	22	AAH44825	PCR primer specific	289	34	3.1	25	21	AAC95582
c 217	35	3.2	30	16	AAQ89019	VSGF 2'-NH2-RNA nu	290	34	3.1	25	21	AAC95629
c 218	35	3.2	30	18	AAQ98807	Primer 63-6 for G	291	34	3.1	25	21	AAC95634
c 219	35	3.2	30	20	AAZ25334	Human chemokine al	292	34	3.1	25	24	ABQ64648
c 220	35	3.2	30	20	AAZ25337	Human chemokine al	293	34	3.1	25	24	ABQ64649
c 221	35	3.2	30	21	AAZ35231	PCR primer RV-C us	c 294	34	3.1	28	16	AAQ83382
c 222	35	3.2	30	22	AAZ35231	Chromobacterium SC	c 295	34	3.1	29	20	AAZ86513
c 223	35	3.2	30	24	ABK49835	Human ADAMTS prote	c 296	34	3.1	29	21	AAZ86513
c 224	35	3.2	31	20	AAZ38868	Human genomic DNA	c 297	34	3.1	29	21	AAZ38868
c 225	35	3.2	31	20	AAZ38868	Human genomic DNA	c 298	34	3.1	30	13	AAQ32894
c 226	35	3.2	31	22	AAZ12735	Human biallelic po	c 299	34	3.1	30	17	AAZ38213
c 227	35	3.2	31	22	AAZ12735	Human alpha-catuli	300	34	3.1	30	19	AAV07145
c 228	35	3.2	32	15	AAQ68918	zebrafish BMP2 cDN	c 301	34	3.1	30	20	AAZ08199
c 229	35	3.2	33	18	AAZ96579	Oligo for C7 elem	c 302	34	3.1	30	20	AAZ08199
c 230	35	3.2	35	21	AAZ92083	Mouse bcl-w gene p	c 303	34	3.1	31	13	AAQ26044
c 231	35	3.2	36	14	AAQ44238	PCR primer for GBP	304	34	3.1	31	13	AAQ26044
c 232	35	3.2	36	16	AAQ80032	ICAM-1 cDNA revers	305	34	3.1	31	19	AAV67982
c 233	35	3.2	36	18	AAZ88977	5' flanking primer	c 306	34	3.1	31	21	AAV01647
c 234	35	3.2	36	20	AAZ87668	Human extracellular	c 307	34	3.1	31	22	AAH49129
c 235	35	3.2	36	20	AAZ87668	Hepatocyte growth	c 308	34	3.1	31	22	AAI29667
c 236	35	3.2	36	22	AAZ56669	PCR primer used to	c 309	34	3.1	31	22	AAI29667
c 237	35	3.2	37	15	AAZ87361	GM-CSF-IgG1-FC dir	c 310	34	3.1	31	22	AAI30774
c 238	35	3.2	37	20	AAZ59193	PCR primer chooldpc	c 311	34	3.1	31	22	AAI30789
c 239	35	3.2	37	20	AAZ79840	Human antibody V-k	c 312	34	3.1	31	22	AAI30859
c 240	35	3.2	37	22	AAH24960	PCR primer FL15405	c 313	34	3.1	31	22	AAI31091
c 241	35	3.2	37	24	ABN89483	PCR primer for hum	c 314	34	3.1	31	22	AAI31091
c 242	35	3.2	37	24	ABK81251	Human obese gene p	c 315	34	3.1	32	20	AAZ60336
c 243	35	3.2	37	24	AAZ19086	Polyimmunoglobulin	c 316	34	3.1	32	20	AAZ21737
c 244	35	3.2	37	24	AAZ19086	Human chorionic go	c 317	34	3.1	33	18	AAZ59388
c 245	35	3.2	38	21	AAZ50458	Oligonucleotide us	c 318	34	3.1	33	20	AAZ83557
c 246	35	3.2	39	21	AAZ50458	Arabidopsis GABA r	c 319	34	3.1	33	24	ABN85721
c 247	35	3.2	39	22	AAZ50458	Clostridium botuli	c 320	34	3.1	33	24	ABN85089
c 248	35	3.2	39	22	AAZ50458	PCR primer for cDN	c 321	34	3.1	33	24	ABL59996
c 249	35	3.2	40	21	AAZ59898	Human IL4Ralpha ge	c 322	34	3.1	34	11	AAQ05011
c 250	34.5	3.1	37	22	AAZ59898	Polynucleotide seq	c 323	34	3.1	34	14	AAQ36325
c 251	34.5	3.1	37	22	AAZ59898	Primer taq82R. Sy	c 324	34	3.1	34	15	AAQ57268
c 252	34	3.1	40	21	AAZ59898	Polynucleotide seq	c 325	34	3.1	35	20	AAQ03931
c 253	34	3.1	17	24	ABL31028	Human HLA genotypi	c 326	34	3.1	35	22	AAQ01940
c 254	34	3.1	17	24	ABL31033	Human HLA genotypi	c 327	34	3.1	35	24	AAZ21088
c 255	34	3.1	18	15	AAQ77633	Ribonucleotide to	c 328	34	3.1	36	14	AAQ36555
c 256	34	3.1	18	15	AAQ77619	Antisense polynuc	c 329	34	3.1	36	21	AAZ35651
c 257	34	3.1	18	15	AAQ77619	Antisense ribonuc	c 330	34	3.1	36	22	AAZ39387
c 258	34	3.1	18	15	AAQ76392	Polynucleotide to	c 331	34	3.1	36	24	AAZ39387
c 259	34	3.1	18	21	AAZ65067	Human bcl genes an	c 332	34	3.1	36	24	ABZ93536
c 260	34	3.1	18	24	ABL30585	Human HLA genotypi	c 333	34	3.1	37	21	AAZ58320
c 261	34	3.1	19	14	AAQ51960	BCL-2 mRNA ribozym	c 334	34	3.1	37	21	AAZ58320
c 262	34	3.1	19	22	AAZ57095	PKCalpha primer-pa	c 335	34	3.1	37	21	AAZ58320
c 263	34	3.1	20	19	AAZ57095	Human Notch3 mutan	c 336	34	3.1	37	22	AAZ58320
c 264	34	3.1	20	21	AAZ46977	Bcl-XL mRNA specif	c 337	34	3.1	37	23	ABK05426
c 265	34	3.1	20	22	AAZ15214	Human bcl-x antise	c 338	34	3.1	37	24	ABN83536
c 266	34	3.1	21	15	AAQ77636	Human bcl-x antise	c 339	34	3.1	38	20	AAZ87562
c 267	34	3.1	21	15	AAQ77636	Ribonucleotide to	c 340	34	3.1	38	22	AAZ15529
c 268	34	3.1	21	15	AAQ77638	Ribonucleotide to	c 341	34	3.1	38	22	AAZ15529
c 269	34	3.1	21	15	AAQ77624	Antisense polynuc	c 342	34	3.1	38	22	AAZ15529
c 270	34	3.1	21	15	AAQ77622	Antisense polynuc	c 343	34	3.1	38	23	ABL58030
c 271	34	3.1	21	15	AAQ77650	Antisense ribonuc	c 344	34	3.1	38	24	AAK98447
c 272	34	3.1	21	15	AAQ77652	Antisense ribonuc	c 345	34	3.1	39	18	AAZ61009
c 273	34	3.1	21	15	AAQ76395	Polynucleotide to	c 346	34	3.1	39	20	AAZ37639
c 274	34	3.1	21	15	AAQ76397	Polynucleotide to	c 347	34	3.1	39	21	AAZ37639
c 275	34	3.1	21	16	AAQ78936	Primer V-R1 for cl	c 348	34	3.1	39	21	AAA69454
c 276	34	3.1	21	21	AAA66244	Dog genomic marker	c 349	34	3.1	39	21	AAA69454
c 277	34	3.1	22	14	AAQ51952	BCL-2 mRNA ribozym	c 350	34	3.1	39	23	ABL58031
c 278	34	3.1	22	18	AAZ48499	Bax omega protein	c 351	34	3.1	39	23	ABA09779
c 279	34	3.1	24	15	AAQ77639	Ribonucleotide to	c 352	34	3.1	39	23	ABA09779
c 280	34	3.1	24	15	AAQ77639	Ribonucleotide to	c 353	34	3.1	39	24	ABL35696
c 281	34	3.1	24	15	AAQ77623	Antisense polynuc	c 354	34	3.1	40	12	AAQ11392
c 282	34	3.1	24	15	AAQ77651	Antisense polynuc	c 355	34	3.1	40	13	AAQ30073
c 283	34	3.1	24	15	AAQ77653	Antisense ribonuc	c 356	34	3.1	40	13	AAQ30862
c 284	34	3.1	24	15	AAQ76396	Antisense ribonuc	c 357	34	3.1	40	19	AAV34466
c 285	34	3.1	24	15	AAQ76396	Polynucleotide to	c 358	34	3.1	40	20	AAZ79333
c 286	34	3.1	24	24	AB186274	Polynucleotide to	c 359	34	3.1	40	20	AAZ79333
						Capture oligonucle						Polynucleotide seq
						HLA DOB gene PCR p						HLA DOB gene PCR p
						HLA DOB gene PCR p						HLA DOB gene PCR p
						HLA DOB gene PCR p						HLA DOB gene PCR p
						Human KTM1a porti						Human KTM1a porti
						c-fos antisense ol						c-fos antisense ol
						Reverse primer use						Reverse primer use
						Polymorphic fragme						Polymorphic fragme
						Human apolipoprote						Human apolipoprote
						PCR primer p20GEX.						PCR primer p20GEX.
						15-Lipoxygenase an						15-Lipoxygenase an
						HTRT sequence-spec						HTRT sequence-spec
						5' PCR primer to a						5' PCR primer to a
						Nucleotide fragmen						Nucleotide fragmen
						Insecticidal gene						Insecticidal gene
						Human genomic DNA						Human genomic DNA
						Human BCKDHB gene						Human BCKDHB gene
						Human single nucle						Human single nucle
						Human single nucle						Human single nucle
						Human single nucle						Human single nucle
						Oligonucleotide #1						Oligonucleotide #1
						PCR primer used in						PCR primer used in
						Competitor oligo A						Competitor oligo A
						Human papilloma vi						Human papilloma vi
						Sweet potato signa						Sweet potato signa
						Human membrane-ass						Human membrane-ass
						Human large protei						Human large protei
						Human Miller-Dieke						Human Miller-Dieke
						Sequence binding t						Sequence binding t
						NGFRpar, targette						NGFRpar, targette
						Enzymatic RNA mole						Enzymatic RNA mole
						PCR primer A from						PCR primer A from
						Linker #2 used in						Linker #2 used in
						Llama sAb gene PC						Llama sAb gene PC
						Encodes linker pep						Encodes linker pep
						Permutate linker e						Permutate linker e
						PKCalpha primer-pa						PKCalpha primer-pa
						Human PDE7A1 3' UT						Human PDE7A1 3' UT
						Hepatitis C virus						Hepatitis C virus
						Human PRO1107 hybr						Human PRO1107 hybr
						Probe used to dete						Probe used to dete
						Human PRO1107 hybr						Human PRO1107 hybr
						Human NOGO G-Cleav						Human NOGO G-Cleav
						C-myc gene target						C-myc gene target
						Human beta-globin						Human beta-globin
						Beta actin gene pr						Beta actin gene pr
						Human manganese su						Human manganese su
						Human beta-globin						Human beta-globin
						Human Inverted CCA						Human Inverted CCA
						Human V gene libra						Human V gene libra
						L-galactono-1,4-la						L-galactono-1,4-la
						HBV detecting prim						HBV detecting prim
						DNA encoding MEK2						DNA encoding MEK2
						Synthetic TMP						

C 360	34	3.1	40	21	AAZ96094	Polynucleotide seq	C 433	33	3.0	25	24	ABN13265	Human GDMLP-1 25-m
C 361	34	3.1	40	21	AAZ96115	Polynucleotide seq	C 434	33	3.0	25	24	ABN13266	Human GDMLP-1 25-m
C 362	34	3.1	40	21	AAZ37327	Human c-kit fragme	C 435	33	3.0	26	18	AAZ70143	Primer pr 887 for
C 363	33.5	3.0	33	18	AAZ85186	Equine rhinovirus	C 436	33	3.0	26	19	AAV56729	Human microsatelli
C 364	33.5	3.0	33	18	AAZ52062	SFI-H3 PCR primer	C 437	33	3.0	26	22	AAV89906	Probe used to iden
C 365	33.5	3.0	36	21	AAQ99063	Cathepsin B substr	C 438	33	3.0	26	23	AAH78691	Mouse procollagen
C 366	33.5	3.0	36	21	AAZ12882	DNA encoding cathe	C 439	33	3.0	26	24	ABQ88539	Human GPCR probe
C 367	33.5	3.0	36	21	AAZ30328	PCR primer 5' VLB5R	C 440	33	3.0	27	9	AAH82286	Probe for DNA enco
C 368	33.5	3.0	39	19	AAV21265	Tissue plasminogen	C 441	33	3.0	27	15	AAQ79234	Guanosine rich oli
C 369	33.5	3.0	40	21	AAZ63513	Thyroid hormone re	C 442	33	3.0	27	17	AAZ72433	GD domain region f
C 370	33.5	3.0	40	22	AAH57145	Human thyroid horm	C 443	33	3.0	27	18	AAZ51652	Viral integrase in
C 371	33	3.0	16	18	AAQ79248	Guanosine rich oli	C 444	33	3.0	27	19	AAZ79236	Oligonucleotide #2
C 372	33	3.0	16	18	AAZ51678	Viral integrase in	C 445	33	3.0	27	20	AAZ27120	Saccharomyces cere
C 373	33	3.0	16	18	AAZ51665	Viral integrase in	C 446	33	3.0	27	20	AAH00491	Human CDC28-#3 RNA
C 374	33	3.0	16	18	AAZ79247	Oligonucleotide #4	C 447	33	3.0	27	22	AAH91288	Human inflammatory
C 375	33	3.0	17	15	AAQ79246	Guanosine rich oli	C 448	33	3.0	27	24	ABQ87922	Enterohaemorrhagic
C 376	33	3.0	17	15	AAQ79233	Guanosine rich oli	C 449	33	3.0	27	24	ABQ87930	Enterohaemorrhagic
C 377	33	3.0	17	18	AAZ51693	Viral integrase in	C 450	33	3.0	27	24	ABQ11182	DNA encoding Bax G
C 378	33	3.0	17	18	AAZ51677	Viral integrase in	C 451	33	3.0	28	20	AAZ09964	Mouse whey acidic
C 379	33	3.0	17	18	AAZ51689	Viral integrase in	C 452	33	3.0	28	20	AAZ55170	Bradykinin recepto
C 380	33	3.0	17	18	AAZ51663	Viral integrase in	C 453	33	3.0	28	20	AAZ55159	Bradykinin recepto
C 381	33	3.0	17	18	AAZ51675	Viral integrase in	C 454	33	3.0	28	21	AAZ20728	Human bradykinin r
C 382	33	3.0	17	18	AAZ51651	Viral integrase in	C 455	33	3.0	28	21	AAZ20739	Human bradykinin r
C 383	33	3.0	17	19	AAZ79268	Oligonucleotide #6	C 456	33	3.0	28	21	AAZ90941	Mutagenic primer f
C 384	33	3.0	17	19	AAZ79270	Oligonucleotide #1	C 457	33	3.0	28	21	AAA34606	Human adenosine re
C 385	33	3.0	17	19	AAZ79208	Oligonucleotide #2	C 458	33	3.0	28	24	ABL49737	Human adenosine re
C 386	33	3.0	17	19	AAZ79235	Oligonucleotide #1	C 459	33	3.0	28	24	AAZ22586	pAM330 mutagenic p
C 387	33	3.0	17	19	AAZ79245	Oligonucleotide #3	C 460	33	3.0	29	18	AAZ02189	PCR primer #7 to i
C 388	33	3.0	17	19	AAZ79256	Oligonucleotide #4	C 461	33	3.0	29	18	AAZ02189	Human foetal liver
C 389	33	3.0	17	19	AAZ79257	Oligonucleotide #5	C 462	33	3.0	29	21	AAZ92450	Type C lectin PCR
C 390	33	3.0	17	20	AAZ28225	Antisense oligonuc	C 463	33	3.0	29	23	ABA02836	Human alpha-2CAR n
C 391	33	3.0	17	20	AAZ23633	Deletion sequence	C 464	33	3.0	30	16	AAQ93284	Family 2 bFGF 2'-N
C 392	33	3.0	17	20	AAZ18754	Target HIV antisen	C 465	33	3.0	30	16	AAQ82630	Chromosome 11 (loc
C 393	33	3.0	17	21	AAZ49365	HIV targetted anti	C 466	33	3.0	30	19	AAV37601	L. seeligeri 3327
C 394	33	3.0	18	15	AAQ79203	Guanosine rich oli	C 467	33	3.0	30	20	AAZ76188	Human Slit-1 PCR p
C 395	33	3.0	18	15	AAQ79231	Guanosine rich oli	C 468	33	3.0	30	21	AAZ99880	Reverse primer pr
C 396	33	3.0	18	15	AAQ79232	Guanosine rich oli	C 469	33	3.0	30	21	AAZ98253	P. oleovirans phac
C 397	33	3.0	18	16	AAZ54754	Mouse IL-5 hammerh	C 470	33	3.0	30	21	AAZ98261	Z. ramigera phbc g
C 398	33	3.0	18	18	AAZ51649	Viral integrase in	C 471	33	3.0	30	22	AAZ56946	FIV-141 proviral g
C 399	33	3.0	18	18	AAZ51650	Viral integrase in	C 472	33	3.0	30	22	AAZ70665	2'NH2 RNA ligand t
C 400	33	3.0	18	18	AAZ51621	Viral integrase in	C 473	33	3.0	30	23	ABL53307	Oligonucleotide li
C 401	33	3.0	18	19	AAZ79212	Oligonucleotide #5	C 474	33	3.0	30	24	ABK91892	Mouse Diff6 PCR pr
C 402	33	3.0	18	19	AAZ79234	Oligonucleotide #2	C 475	33	3.0	30	24	ABK12581	Blue light recepto
C 403	33	3.0	20	19	AAV41288	Antisense oligo ma	C 476	33	3.0	31	15	AAQ74330	Human Igg-1 light
C 404	33	3.0	20	20	AAZ56438	Mouse vWF PCR reve	C 477	33	3.0	31	16	AAQ76237	Primer for ampli
C 405	33	3.0	20	21	AAZ55049	Human bcl genes an	C 478	33	3.0	31	18	AAV05354	PCR primer used to
C 406	33	3.0	20	22	AAH44820	Antisense oligonuc	C 479	33	3.0	31	18	AAZ97361	Construction of pl
C 407	33	3.0	20	22	AAZ43896	Human chromosome 1	C 480	33	3.0	31	19	AAV36712	Nucleotide sequenc
C 408	33	3.0	21	16	AAQ94296	Recombinant C. his	C 481	33	3.0	31	20	AAZ38848	Human genomic DNA
C 409	33	3.0	21	16	AAQ94297	Recombinant C. his	C 482	33	3.0	31	20	AAZ99479	PCR primer and pro
C 410	33	3.0	21	17	AAZ35037	Triplex-forming ol	C 483	33	3.0	31	20	AAV68129	Oligonucleotide us
C 411	33	3.0	21	21	AAZ59809	Primer for Bcl-X n	C 484	33	3.0	31	22	AAI30234	Human single nucle
C 412	33	3.0	21	22	AAH41791	Bcl-X gene PCR pri	C 485	33	3.0	31	22	AAI30998	Human single nucle
C 413	33	3.0	21	22	AAZ96909	Human gene single	C 486	33	3.0	31	22	AAH97241	Human Chk1 ribozym
C 414	33	3.0	21	22	AAZ98514	Human cytochrome P	C 487	33	3.0	31	22	AAH43465	cdNA clone HP03564
C 415	33	3.0	22	18	AAZ63192	FSH receptor fshr	C 488	33	3.0	31	23	ABZ97861	Non-endogenous hum
C 416	33	3.0	23	14	AAQ48964	HepG2 histidyl trn	C 489	33	3.0	31	23	ABZ97862	Non-endogenous hum
C 417	33	3.0	23	18	AAZ89668	Human histidyl-trn	C 490	33	3.0	31	24	ABK67729	Novel transglutami
C 418	33	3.0	24	21	AAZ95425	Cat flea HMT ligan	C 491	33	3.0	31	24	ABK67736	Novel transglutami
C 419	33	3.0	24	24	ABA04772	F-cassette structu	C 492	33	3.0	31	24	AAZ17784	Human Igg1 light c
C 420	33	3.0	25	21	AAZ36647	PCR primer VDE119	C 493	33	3.0	32	18	AAZ90919	Primer for Von Hip
C 421	33	3.0	25	22	AAH38031	SNP specific SNPE	C 494	33	3.0	32	18	AAZ94902	Reverse primer for
C 422	33	3.0	25	24	ABQ64651	Human KTM1a porti	C 495	33	3.0	32	19	AAV18034	PrMADS2 promoter r
C 423	33	3.0	25	24	ABQ64652	Human KTM1a porti	C 496	33	3.0	32	20	AAZ38066	RGH nucleic acid g
C 424	33	3.0	25	24	ABQ64654	Human KTM1a porti	C 497	33	3.0	32	20	AAZ38066	Retrovirus RGH gag
C 425	33	3.0	25	24	ABQ64655	Human KTM1a porti	C 498	33	3.0	32	22	AAZ19089	Retrovirus RGH gag
C 426	33	3.0	25	24	ABN033934	Human GDMLP-1 25-m	C 499	33	3.0	32	22	AAZ19099	HERV-H/RGH retrovi
C 427	33	3.0	25	24	ABN033935	Human GDMLP-1 25-m	C 500	33	3.0	32	22	AAH76874	Mouse mas-like (ML
C 428	33	3.0	25	24	ABN04421	Human GDMLP-1 25-m	C 501	33	3.0	32	22	ABK96452	PCR primer OGR38 f
C 429	33	3.0	25	24	ABN04422	Human GDMLP-1 25-m							
C 430	33	3.0	25	24	ABN13262	Human GDMLP-1 25-m							
C 431	33	3.0	25	24	ABN13263	Human GDMLP-1 25-m							
C 432	33	3.0	25	24	ABN13264	Human GDMLP-1 25-m							

ALIGNMENTS

RESULT 1

AAQ51961
ID AAQ51961 standard; RNA; 36 BP.
XX
AC AAQ51961;
XX
DT 26-MAY-1994 (first entry)
XX
DE BCL-2 mRNA ribozyme cleavable nucleotide (1997).
XX
KW Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
KW human; chronic myelogenous leukemia; CML; follicular lymphoma;
KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
KW hairpin; hepatitis delta virus; group I intron; RNaseP; ss.
XX
NS Homo sapiens.
XX
PN WO9323057-A.
XX
PD 25-NOV-1993.
XX
PF 13-MAY-1993; 93WO-US04573.
XX
PR 14-MAY-1992; 92US-0882822.
PR 14-MAY-1992; 92US-0882885.
PR 26-AUG-1992; 92US-0936110.
PR 26-AUG-1992; 92US-0936421.
PR 26-AUG-1992; 92US-0936422.
PR 26-AUG-1992; 92US-0936531.
PR 26-AUG-1992; 92US-0936532.
PR 07-DEC-1992; 92US-0987131.
PR 19-JAN-1993; 93US-0006122.
PR 19-JAN-1993; 93US-0008910.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Draper KG, Thompson JD;
XX
DR WPT; 1993-386203/48.
XX
PT New enzymatic RNA molecules (ribozymes) - which cleave mRNA
PT associated with tumours or mRNA expressed from gene encoding
PT multiple drug resistance
XX
PS Claim 3; Fig 6; 69pp; English.
XX
CC The sequences given in AAQ51825-2266 represent areas of mRNAs which are
CC associated with development or maintenance of chronic myelogenous
CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or
CC acute lymphocytic leukemia, follicular lymphoma, B-cell acute
CC lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma
CC and lung cancer. The full length mRNAs containing these target
CC sequences, encode aberrant cellular proteins which are able to control
CC cellular proliferation and are directly linked to a leukemic
CC phenotype. These target sequences are identified by the ribozyme of
CC the invention. The ribozymes is formed in a hammerhead motif, but may
CC also be formed in the motif of a hairpin, hepatitis delta virus, group
CC I intron or RNaseP-like RNA. These ribozymes may be used to inhibit
CC the development or expression of a transformed phenotype in man and
CC other animals by modulating expression of the corresponding gene.
CC Cleavage of target mRNAs expressed in pre-neoplastic and transformed
CC cells elicits inhibition of the transformed state. Multiple drug
CC resistance (mdr-1) mRNA specific ribozymes remove the mechanism of
CC drug resistance used by transformed cells and thus enhances drug
CC therapies for tumours. The ribozymes may also be used to study
CC genetic drift and mutations within cells.
XX
SQ Sequence 36 BP; 10 A; 13 C; 8 G; 5 U; 0 other;
XX
Alignment Scores:

Pred. No.: 1.59e+03 Length: 36
Score: 66.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.98% Indels: 0
DB: 14 Gaps: 0
US-09-375-514-22 (1-205) x AAQ51961 (1-36)
QY 181 LeuAsnArgHisLeuHisThrTrpIleGlnAsp 191
Db 3 CUGAACCGGCACCCUGCACCUGGAUCCAGGAU 35
RESULT 2
AAQ51951
ID AAQ51951 standard; RNA; 33 BP.
XX
AC AAQ51951;
XX
DT 26-MAY-1994 (first entry)
XX
DE BCL-2 mRNA ribozyme cleavable nucleotide (1592).
XX
KW Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
KW human; chronic myelogenous leukemia; CML; follicular lymphoma;
KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
KW hairpin; hepatitis delta virus; group I intron; RNaseP; ss.
XX
OS Homo sapiens.
XX
PN WO9323057-A.
XX
PD 25-NOV-1993.
XX
PF 13-MAY-1993; 93WO-US04573.
XX
PR 14-MAY-1992; 92US-0882822.
PR 14-MAY-1992; 92US-0882885.
PR 26-AUG-1992; 92US-0936110.
PR 26-AUG-1992; 92US-0936421.
PR 26-AUG-1992; 92US-0936422.
PR 26-AUG-1992; 92US-0936531.
PR 26-AUG-1992; 92US-0936532.
PR 07-DEC-1992; 92US-0987131.
PR 19-JAN-1993; 93US-0006122.
PR 19-JAN-1993; 93US-0008910.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Draper KG, Thompson JD;
XX
DR WPT; 1993-386203/48.
XX
PT New enzymatic RNA molecules (ribozymes) - which cleave mRNA
PT associated with tumours or mRNA expressed from gene encoding
PT multiple drug resistance
XX
PS Claim 3; Fig 6; 69pp; English.
XX
CC The sequences given in AAQ51825-2266 represent areas of mRNAs which are
CC associated with development or maintenance of chronic myelogenous
CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or
CC acute lymphocytic leukemia, follicular lymphoma, B-cell acute
CC lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma
CC and lung cancer. The full length mRNAs containing these target
CC sequences, encode aberrant cellular proteins which are able to control
CC cellular proliferation and are directly linked to a leukemic
CC phenotype. These target sequences are identified by the ribozyme of
CC the invention. The ribozymes is formed in a hammerhead motif, but may

CC also be formed in the motif of a hairpin, hepatitis delta virus, group
 CC I intron or RNasep-like RNA. These ribozymes may be used to inhibit
 CC the development or expression of a transformed phenotype in man and
 CC other animals by modulating expression of the corresponding gene.
 CC Cleavage of target mRNAs expressed in pre-neoplastic and transformed
 CC cells elicits inhibition of the transformed state. Multiple drug
 CC resistance (mdr-1) mRNA specific ribozymes remove the mechanism of
 CC drug resistance used by transformed cells and thus enhances drug
 CC therapies for tumours. The ribozymes may also be used to study
 CC genetic drift and mutations within cells.

XX SQ Sequence 33 BP; 5 A; 16 C; 7 G; 5 U; 0 other;

Alignment Scores:
 Pred. No.: 5.79e+03 Length: 33
 Score: 57.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.16% Indels: 0
 DB: 14 Gaps: 0

US-09-375-514-22 (1-205) x AAQ51951 (1-33)

Qy 46 ProGlyIlePheSerSerGlnProGlyHis 55

Db 3 CCGGGCAUCUUCUCCAGCCAGCCGGGCAC 32

RESULT 3

AAV28336/C

ID AAV28336 standard; cDNA; 24 BP.

XX AC AAV28336;

XX DT 02-OCT-1998 (first entry)

XX DE Rat bcl-y downstream primer.

XX KW ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat;

XX KW PCR; primer; amplification.

XX OS Synthetic.

XX OS Rattus sp.

XX PN US789201-A.

XX PD 04-AUG-1998.

XX PF 11-FEB-1997; 97US-0798897.

XX PR 23-FEB-1996; 96US-0012201.

XX PR 11-FEB-1997; 97US-0798897.

XX PA (COCE-) COCENSYS INC.

XX PI Guastella J;

XX DR WPI; 1998-446079/38.

XX PT Nucleic acids encoding B-cell lymphoma-y protein - useful for
 PT producing recombinant protein for use in treating uncontrolled cell
 PT growth e.g. cancers

XX PS Example; Column 11; 27pp; English.

XX CC The primers AAV28335 and AAV28336 were used to amplify the rat bcl-y
 CC gene. The mammalian bcl-y genes encode a protein that is a member of the
 CC bcl-2 family, components in the cell death pathway. The bcl-2 family
 CC have both apoptotic activity and the apoptosis blocking activity. bcl-y
 CC falls in the apoptosis activity category. The recombinant protein may
 CC be used to prevent uncontrolled cell growth, either by its direct
 CC administration to recombinant genetic constructs to increase its
 CC expression in vivo. Also, antisense constructs can be used in disorders
 CC where prevention of cell death is desired.

XX SQ Sequence 24 BP; 3 A; 9 C; 1 G; 5 T; 6 other;

Alignment Scores:
 Pred. No.: 5.66e+03 Length: 24
 Score: 55.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.98% Indels: 0
 DB: 19 Gaps: 0

US-09-375-514-22 (1-205) x AAV28336 (1-24)

Qy 188 TrpIleGlnAspAsnGlyGlyTrp 195

Db 24 TGGATCCARGAYAAAYGGNGTGG 1

RESULT 4

AAAX15948/C

ID AAX15948 standard; DNA; 24 BP.

XX AC AAX15948;

XX DT 20-MAY-1999 (first entry)

XX DE PCR primer used to amplify cDNA encoding the rat bcl-y protein.

XX KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW premature cell death; cell death stimulator; prolonged cell life span;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
 KW parasite; PCR primer; ss.

XX OS Synthetic.

XX OS Rattus sp.

XX PN US5883229-A.

XX PD 16-MAR-1999.

XX PF 25-NOV-1997; 97US-0978523.

XX PR 23-FEB-1996; 96US-0012201.

XX PR 11-FEB-1997; 97US-0798897.

XX PR 25-NOV-1997; 97US-0978523.

XX PA (COCE-) COCENSYS INC.

XX PI Guastella J;

XX DR WPI; 1999-214150/18.

XX PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
 PT for modulating programmed cell death

XX PS Example 1; Columns 11; 26pp; English.

XX CC PCR primers AAX15947-48 were used to amplify cDNA encoding rat bcl-y
 CC protein (Rbcl-y). The specification also describes human bcl-y protein
 CC (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought
 CC to be involved in programmed cell death (apoptosis and necrosis). Rbcl-y
 CC and Hbcl-y proteins may be used to treat conditions associated with a
 CC disruption of the cell death pathway. If they act as cell death
 CC inhibitors, they may be used in therapies to treat subjects suffering
 CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
 CC degenerative diseases (especially multiple sclerosis), myocardial
 CC infarction, vitally induced cell death, aging, spinal cord injuries and
 CC amyotrophic lateral sclerosis- conditions where cells under go premature
 CC cell death as a result of triggers which may or may not be apparent.
 CC They may also be used in this way to develop cell lines which remain

CC viable in culture for an extended period. In contrast, if they act as
 CC cell death stimulators, Bcl-2 and Bcl-x may be used to treat conditions
 CC associated with prolonged cell life span such as cancer (especially
 CC kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may
 CC also be used to cause cell death in, and hence control, parasites.
 XX

SQ Sequence 24 BP; 3 A; 9 C; 1 G; 5 T; 6 other;

Alignment Scores:

Pred. No.: 24
 Score: 5.66e+03 Length: 24
 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.98% Indels: 0
 DB: 20 Gaps: 0

US-09-375-514-22 (1-205) x AAI15948 (1-24)

Y 188 TptleGlnAspAsnGlyGlyTrp 195

Db 24 TGGATCARGAYATGGGNGTGG 1

RESULT 5

AAI64676/c

ID AAI64676 standard; DNA; 33 BP.

AC AAI64676;

DT 04-DEC-2001 (first entry)

DE Human proteolytic enzyme regulatory protein 12 PCR primer 3.

KW Human; proteolytic enzyme regulatory protein 12; cytostatic; virucidal;
 KW immunomodulatory; antiinflammatory; haemostatic; malignant tumour; HIV;
 KW infection; human immunodeficiency virus; immunological disease;
 KW PCR primer; ss.

OS Homo sapiens.

PN WO200172793-A1.

XX 04-OCT-2001.

XX 26-MAR-2001; 2001WO-CN00476.

XX 28-MAR-2000; 2000CN-0115200.

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX Mao Y, Xie Y;

XX WPI; 2001-597100/67.

XX New human proteolytic enzyme regulatory protein 12 and encoded
 PT polynucleotide, applicable in diagnosis and treatment of cancer,
 PT haemopathy, human immunodeficiency virus infection, immunological
 PT diseases and inflammation

XX Example 4; Page 16; 34pp; Chinese.

XX The invention relates to human proteolytic enzyme regulatory protein 12
 CC with cytostatic, virucidal, immunomodulatory, antiinflammatory and
 CC haemostatic activity. The polypeptide and encoded polynucleotide are
 CC applicable in diagnosis and treatment of malignant tumour, haemopathy,
 CC HIV infection, immunological diseases and various inflammations. The
 CC present sequence is that of a human proteolytic enzyme regulatory protein
 CC 12 PCR primer, useful to the invention.

SQ Sequence 33 BP; 8 A; 5 C; 7 G; 13 T; 0 other;

Alignment Scores:

Pred. No.: 33 Length: 33
 Score: 1.69e+04 Matches: 8
 50.00

Percent Similarity: 88.89% Conservative: 0
 Best Local Similarity: 88.89% Mismatches: 1
 Query Match: 4.53% Indels: 0
 DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x AAI64676 (1-33)

QY 181 LeuAsnArgHisLeuHisThrTrpIle 189

Db 31 TTAAATAGGCATACACACATGGATC 5

RESULT 6

AAH45307

ID AAH45307 standard; DNA; 36 BP.

XX AAH45307;

XX 10-SEP-2001 (first entry)

XX Human Bcl-2 PCR primer oligo-10.

KW Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; PCR primer; ss.

OS Homo sapiens.

PN WO200142459-A1.

XX 14-JUN-2001.

XX 07-DEC-2000; 2000WO-JP08667.

XX 09-DEC-1999; 99JP-0350427.

XX (HISM) HISAMITSU PHARM CO LTD.

XX Shibazaki F, Kuma H;

XX WPI; 2001-381681/40.

XX New apoptosis inhibitors, useful for treating apoptosis related
 PT disorders

XX Example 1; Page 39; 43pp; Japanese.

XX The invention relates to an apoptosis inhibitor comprising the
 CC amino acid sequence of Bcl-2 protein in which at least one serine
 CC residue is substituted by alanine or aspartic acid. The protein has
 CC increased apoptosis inhibitory activity compared with the wild type
 CC Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment
 CC of disorders caused by apoptosis. The present sequence was used to
 CC amplify DNA encoding the human Bcl-2 protein.

SQ Sequence 36 BP; 7 A; 10 C; 15 G; 4 T; 0 other;

Alignment Scores:

Pred. No.: 1.85e+04 Length: 36
 Score: 50.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.53% Indels: 0
 DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x AAH45307 (1-36)

QY 1 MetAlaHisAlaGlyArgThrGlyTyr 9

Db 10 ATGGCGCACGCTGGGAGAACGGGTAC 36

RESULT 7

ABN85362/c

ID ABN85362 standard; DNA; 24 BP.

XX ABN85362;

XX 07-OCT-2002 (first entry)
XX Bcl-2 related oligonucleotide #3.
XX Interferon; cytokine; alpha-1 interferon; beta-1 interferon; Bcl-2;
XX gamma-1 interferon; interferon-regulated enzyme; ds-protein kinase;
XX 2',5'-oligoadenylatesynthetase; RNAase L; Fas antigen;
XX gamma-actin cytoskeleton protein; ss.
XX Unidentified.
XX RU2181773-C2.
XX 27-APR-2002.
XX 16-MAR-2000; 2000RU-0106253.
XX 16-MAR-2000; 2000RU-0106253.
XX (AMVI-) A MED VIROLOGY RES INST.
XX Sokolova TM, Uryvaev LV;
XX WPI; 2002-391288/42.
XX Method of assay of human cytokine status at genetic level
XX Claim 1; Page 7; 10pp; Russian.
XX The present invention relates to a method for estimating transcription
XX levels of genes encoding interferons, interferon-dependent and
XX proliferative cytokines. The method involves determining cytokine mRNA
XX levels, using a combination of RT-PCR with blot- and dot-hybridisation.
XX To illustrate the method, cytokines (alpha-1, beta-1 and gamma-1
XX interferon), interferon-regulated enzymes
XX (2',5'-oligoadenylatesynthetase, RNAase L and ds-protein kinase) and
XX factors of cellular proliferation (Bcl-2, Fas antigen and gamma-actin
XX cytoskeleton protein) were used. The present oligonucleotide was used to
XX illustrate the invention.
XX SQ Sequence 24 BP; 2 A; 15 C; 2 G; 5 T; 0 other;
Alignment Scores:
Pred. No.: 1.42e+04 Length: 24
Score: 49.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.44% Indels: 0
DB: 24 Gaps: 0
US-09-375-514-22 (1-205) x ABN85362 (1-24)
QY 139 ArgAspGlyValAsnTrpGlyArg 146
Db 24 AGGACGGGGTGAACCTGGGGAGG 1
RESULT 8
ABN85361/C
ID ABN85361 standard; DNA; 21 BP.
XX AC ABN85361;
XX 07-OCT-2002 (first entry)
XX Bcl-2 related oligonucleotide #2.
XX Interferon; cytokine; alpha-1 interferon; beta-1 interferon; Bcl-2;
XX gamma-1 interferon; interferon-regulated enzyme; ds-protein kinase;
XX 2',5'-oligoadenylatesynthetase; RNAase L; Fas antigen;
XX gamma-actin cytoskeleton protein; ss.
XX Unidentified.

XX RU2181773-C2.
XX 27-APR-2002.
XX 16-MAR-2000; 2000RU-0106253.
XX 16-MAR-2000; 2000RU-0106253.
XX (AMVI-) A MED VIROLOGY RES INST.
XX Sokolova TM, Uryvaev LV;
XX WPI; 2002-391288/42.
XX Method of assay of human cytokine status at genetic level
XX Claim 1; Page 7; 10pp; Russian.
XX The present invention relates to a method for estimating transcription
XX levels of genes encoding interferons, interferon-dependent and
XX proliferative cytokines. The method involves determining cytokine mRNA
XX levels, using a combination of RT-PCR with blot- and dot-hybridisation.
XX To illustrate the method, cytokines (alpha-1, beta-1 and gamma-1
XX interferon), interferon-regulated enzymes
XX (2',5'-oligoadenylatesynthetase, RNAase L and ds-protein kinase) and
XX factors of cellular proliferation (Bcl-2, Fas antigen and gamma-actin
XX cytoskeleton protein) were used. The present oligonucleotide was used to
XX illustrate the invention.
XX SQ Sequence 21 BP; 2 A; 5 C; 9 G; 5 T; 0 other;
Alignment Scores:
Pred. No.: 1.68e+04 Length: 21
Score: 47.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.26% Indels: 0
DB: 24 Gaps: 0
US-09-375-514-22 (1-205) x ABN85361 (1-21)
QY 182 AsnArgHisLeuHisThrTrp 188
Db 21 AACCGGCACCTGCACACCTGG 1
RESULT 9
AAQ86646
ID AAQ86646 standard; DNA; 33 BP.
XX AC AAQ86646;
XX 27-SEP-1995 (first entry)
XX Bcl-2 splice donor site.
XX Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
XX leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;
XX ss.
XX Synthetic.
XX WO9508350-A.
XX 30-MAR-1995.
XX 20-SEP-1994; 94WO-US10725.
XX 20-SEP-1993; 93US-0124256.
XX (REED/) REED J C.
XX Reed JC;
PI

XX WPI; 1995-139394/18.
 XX
 PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
 of human solid tumours, esp. breast cancer
 XX
 XX Disclosure; Page 13; 108pp; English.

XX The antisense oligonucleotide SD-AS (AAQ86645) is complementary to a
 portion of the splice donor site of the pre-mRNA coding strand of the
 human bcl-2 gene. It reduces the expression of bcl-2 gene product,
 thereby inducing programmed cell death of certain cancer cells. The
 corresp. bcl-2 sense splice donor site region was synthesized for use
 as a control.

XX Sequence 33 BP; 5 A; 5 C; 16 G; 7 T; 0 other;

Alignment Scores:
 Pred. No.: 2.68e+04 Length: 33
 Score: 47.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.26% Indels: 0
 DB: 16 Gaps: 0

US-09-375-514-22 (1-205) x AAQ86646 (1-33)

QY 193 GlyGlyTrpValGlyAlaSerGly 200
 ID AAV19654 standard; DNA; 33 BP.
 AC AAV19654;
 XX
 DT 12-JUN-1998 (first entry)
 DE Human bcl-2 oligonucleotide 2.

XX Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
 cancer; ss.
 OS Synthetic.
 OS Homo sapiens.
 XX US5734033-A.
 XX 31-MAR-1998.
 XX 24-MAR-1994; 94US-0288692.
 XX 21-FEB-1992; 92US-0840716.
 XX 22-DEC-1988; 88US-0288692.
 XX 24-MAR-1994; 94US-0217082.
 XX (UIPE-) UNIV PENNSYLVANIA.
 XX Reed J;
 XX WPI; 1998-229881/20.

XX Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
 for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
 XX
 XX Disclosure; Columns 3-4; 21pp; English.

XX This is a human bcl-2 oligonucleotide based on which an antisense
 oligonucleotide complementary to the splice donor site of the human
 bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides straddle
 strategic sites such as the translation initiation site, donor and
 acceptor splicing sites, or sites for transportation or degradation.

CC Blocking translation at such strategic sites prevents the formation of a
 functional bcl-2 gene product. These oligonucleotides may be used for
 CC treating cancers associated with high levels of bcl-2 gene expression,
 CC especially lymphomas and some leukaemias.

XX Sequence 33 BP; 5 A; 5 C; 16 G; 7 T; 0 other;

Alignment Scores:
 Pred. No.: 2.68e+04 Length: 33
 Score: 47.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.26% Indels: 0
 DB: 19 Gaps: 0

US-09-375-514-22 (1-205) x AAV19654 (1-33)

QY 193 GlyGlyTrpValGlyAlaSerGly 200
 ID AAV19654 standard; DNA; 33 BP.
 AC AAV19654;
 XX
 DT 12-JUL-2002 (first entry)
 DE Bcl-2 antisense oligonucleotide.

XX B cell lymphoma/leukaemia-2; bcl-2; oncogene; antisense; lymphoma;
 KW leukaemia; colon carcinoma; rectal carcinoma; pancreatic cancer;
 KW breast cancer; ovarian cancer; prostate cancer; renal cell carcinoma;
 KW hepatoma; bile duct carcinoma; choriocarcinoma; cervical cancer;
 KW testicular cancer; lung carcinoma; bladder carcinoma; melanoma;
 KW head and neck cancer; brain cancer; cytostatic; human; gene therapy;
 ss.

XX Homo sapiens.

XX WO200217852-A2.

XX 07-MAR-2002.

XX 23-AUG-2001; 2001WO-US26414.

XX 25-AUG-2000; 2000US-227970P.

XX 29-SEP-2000; 2000US-237009P.

XX 10-NOV-2000; 2000US-0709170.

XX (GENT-) GENTA INC.

XX Warrel RP, Klem RE, Fingert H;

XX WPI; 2002-371796/40.

XX Treating or preventing cancer, tumors and carcinomas, comprises
 administering B cell lymphoma/leukemia-2 antisense oligonucleotide at
 high doses for short period for time with one or more cancer
 therapeutics -

XX Disclosure; Page 53; 64pp; English.

XX The present sequence is that of a B cell lymphoma/leukaemia-2
 (bcl-2) antisense oligonucleotide. The present invention is
 CC directed to the use of bcl-2 antisense oligomers, particularly
 CC G3139 (see ABL54148), to treat and prevent bcl-2 related disorders.
 CC Administration at high doses results in significant therapeutic
 CC responses, including low toxicity, high tolerance and prolonged
 CC survival. Administration at high doses for short periods of time
 CC (less than 14 days) also provides significant therapeutic responses
 CC in the treatment of cancer. The bcl-2 antisense oligomer may also

CC be used to increase the sensitivity of a subject to cancer
 CC therapeutics, and in combination with hormone treatment or gene
 CC therapy. Conditions that may be treated or prevented include
 CC cancer of the haematopoietic system, skin, bone and soft tissue,
 CC reproductive system, genitourinary system, breast, endocrine
 CC system, brain, central nervous system, peripheral nervous system,
 CC kidney, lung, respiratory system, thorax, gastrointestinal and
 CC alimentary canal, lymph nodes, pancreas, hepatobiliary system, or
 CC cancer of unknown primary site, non-Hodgkin's lymphoma, Hodgkin's
 CC lymphoma, leukaemia, colon carcinoma, rectal carcinoma, pancreatic
 CC breast, ovarian, prostate, cervical, testicular, head and neck or
 CC brain cancer, renal cell carcinoma, hepatoma, bile duct carcinoma,
 CC choriocarcinoma, lung carcinoma, bladder carcinoma and melanoma
 CC (all claimed).

SQ Sequence 33 BP; 5 A; 5 C; 16 G; 7 T; 0 other;

Alignment Scores:
 Pred. No.: 2.68e+04 Length: 33
 Score: 47.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.26% Indels: 0
 DB: 24 Gaps: 0

US-09-375-514-22 (1-205) x ABL54152 (1-33)

QY 193 GlyGlyTrpValGlyAlaSerGly 200

DB 10 GGAGCGTGGTAGGTGCATCTGGT 33

RESULT 12

AAQ51954

ID AAQ51954 standard; RNA; 28 BP.

AC AAQ51954;

DT 26-MAY-1994 (first entry)

XX BCL-2 mRNA ribozyme cleavable nucleotide (1729).

XX Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
 KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
 KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
 KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
 KW human; chronic myelogenous leukemia; CML; follicular lymphoma;
 KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
 KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
 KW hairpin; hepatitis delta virus; group I intron; RNaseP; ss.

XX Homo sapiens.

XX WO9323057-A.

XX 25-NOV-1993.

XX 13-MAY-1993; 93WO-US04573.

XX 14-MAY-1992; 92US-0882822.

XX 14-MAY-1992; 92US-0882885.

XX 26-AUG-1992; 92US-0936110.

XX 26-AUG-1992; 92US-0936421.

XX 26-AUG-1992; 92US-0936422.

XX 26-AUG-1992; 92US-0936531.

XX 07-DEC-1992; 92US-0936532.

XX 19-JAN-1993; 92US-0987131.

XX 19-JAN-1993; 92US-0006122.

XX 19-JAN-1993; 93US-0008910.

XX (RIBO-) RIBOZYME PHARM INC.

XX Draper KG, Thompson JD;

XX

DR WPI; 1993-386203/48.

XX New enzymatic RNA molecules (ribozymes) - which cleave mRNA
 PT associated with tumours or mRNA expressed from gene encoding
 PT multiple drug resistance

XX Claim 3; Fig 6; 69pp; English.

XX The sequences given in AAQ51825-2266 represent areas of mRNAs which are
 CC associated with development or maintenance of chronic myelogenous
 CC leukemia (CML); promyelocytic leukemia, Burkitt's lymphoma, or
 CC acute lymphocytic leukemia, follicular lymphoma, B-cell acute
 CC lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma
 CC and lung cancer. The full length mRNAs containing these target
 CC sequences, encode aberrant cellular proteins which are able to control
 CC cellular proliferation and are directly linked to a leukemic
 CC phenotype. These target sequences are identified by the ribozyme of
 CC the invention. The ribozymes is formed in a hammerhead motif, but may
 CC also be formed in the motif of a hairpin, hepatitis delta virus, group
 CC I intron or RNaseP-like RNA. These ribozymes may be used to inhibit
 CC the development or expression of a transformed phenotype in man and
 CC other animals by modulating expression of the corresponding gene.
 CC Cleavage of target mRNAs expressed in pre-neoplastic and transformed
 CC cells elicits inhibition of the transformed state. Multiple drug
 CC resistance (mdr-1) mRNA specific ribozymes remove the mechanism of
 CC drug resistance used by transformed cells and thus enhances drug
 CC therapies for tumours. The ribozymes may also be used to study
 CC genetic drift and mutations within cells.

XX Sequence 28 BP; 3 A; 13 C; 7 G; 5 U; 0 other;

Alignment Scores:

Pred. No.: 3.08e+04 Length: 28
 Score: 45.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.08% Indels: 0
 DB: 14 Gaps: 0

US-09-375-514-22 (1-205) x AAQ51954 (1-28)

QY 91 ProValValHisLeuAlaLeuArgGln 99

DB 1 CCUGUGUGUCCACCGUGCCGCCGCCCAA 27

RESULT 13

AAAT36054/C

ID AAT36054 standard; DNA; 24 BP.

XX AAT36054;

XX 20-NOV-1996 (first entry)

XX bcl-2 reverse PCR primer.

XX Cardiovascular disease; differential expression; target gene;

XX pathway gene; fingerprint gene; atherosclerosis; ischaemia;

XX reperfusion; hypertension; restenosis; arterial inflammation;

XX vector; antibody; diagnosis; gene therapy; drug screening;

XX bcl-2; polymerase chain reaction; PCR; primer; ss.

XX Synthetic.

XX WO9624604-A1.

XX 15-AUG-1996.

XX 09-FEB-1996; 96WO-US01883.

XX 07-JUN-1995; 95US-0485573.

XX 10-FEB-1995; 95US-0386844.

XX (MILL-) MILLENNIUM PHARM INC.

XX Falb DA;
 PI WPI; 1996-384391/38.
 XX
 XX New genes differentially expressed in cardiovascular disease - and
 PT related vectors, host cells, proteins and antibodies, for diagnosis,
 PT monitoring, treatment and drug screening
 XX
 PS Example 7; Page 12; 200pp; English.

XX Monocyte RNA from apolipoprotein E (apoE)-deficient and control
 CC mice was compared using primers for mouse bcl-2 (AAT36053 and
 CC AAT36054) and gamma-actin (AAT36055 and AAT36056). bcl-2 mRNA
 CC levels were significantly lower in the apoE-deficient mice (an
 CC animal model of atherosclerosis). Regulation of the mouse bcl-2
 CC gene appeared to be regulated by serum cholesterol levels.
 CC Similar results were obtained with the human bcl-2 and glutathione
 CC peroxidase genes (see also AAT36057-58). The discovery that certain
 CC genes (see also AAT26029-36) are differentially expressed in
 CC cardiovascular diseases can be used to develop methods for the
 CC diagnosis and treatment of such diseases.

XX Sequence 24 BP; 4 A; 14 C; 1 G; 5 T; 0 other;

Alignment Scores:
 Pred. No.: 3.06e+04 Length: 24
 Score: 44.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.99% Indels: 0
 DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x AAT36054 (1-24)

QY 140 AspGlyValAsnTrpGlyArg 146

Db 23 GATGGGTGAACCTGGGGAGG 3

RESULT 14

AAV26250/c
 ID AAV26250 standard; DNA; 24 BP.

XX AAV26250;

XX 24-MAY-1999 (first entry)

XX Reverse primer for RT-PCR analysis of mouse bcl-2 mRNA.

XX Fingerprinting gene; rchd502; transmembrane protein; cardiovascular;
 KW fingerprint/target gene; up-regulated; endothelial cell; shear-stress;
 KW atherosclerosis; ischemia; reperfusion; hypertension; restenosis; human;
 KW RT-PCR; primer; bcl-2; mouse; ss.

XX Synthetic.

OS Mus sp.

XX US5882925-A.

XX 16-MAR-1999.

XX 09-FEB-1996; 96US-0599654.

XX 09-FEB-1996; 96US-0599654.

XX 10-FEB-1995; 95US-0386844.

XX 07-JUN-1995; 95US-0485573.

XX (MILL-) MILLENNIUM PHARM INC.

XX Falb DA;

XX WPI; 1999-214071/18.

XX

PT New polynucleotides consisting of residues 1-1929 of the rchd502
 PT gene - are differentially expressed in cardiovascular disease
 PT states, and can therefore be used to treat and diagnose
 PT cardiovascular diseases

XX Disclosure; Column 9; 121pp; English.

XX The invention relates to a rchd502 target/fingerprint gene encoding a
 CC transmembrane protein. The invention provides cDNAs contained in plasmids
 CC pCHD502SF (ATCC 6981) and pCHD502SJ (ATCC 6982) that encode the
 CC rchd502 polypeptide, and are differentially expressed in cardiovascular
 CC disease states. Cultured genetically engineered host cell containing the
 CC rchd502 polynucleotides in operative association with a nucleotide
 CC regulatory element are used for producing a polypeptide rchd502 gene
 CC product. Identifying that the fingerprint/target gene rchd502 is
 CC differentially expressed (up-regulated) by endothelial cells subjected
 CC to shear stress, provides a tool for the diagnosis and treatment of
 CC cardiovascular disease e.g. atherosclerosis, ischemia/reperfusion,
 CC hypertension, restenosis. The fingerprint gene is useful for testing the
 CC efficacy of candidate drugs in basic research and in clinical trials and
 CC or imaging of a diseased cardiovascular tissue. The gene may also be
 CC used in screening for ligands of target gene product receptor domains, as
 CC well as antagonists of the ligand-receptor interaction.

XX Sequence 24 BP; 4 A; 14 C; 1 G; 5 T; 0 other;

Alignment Scores:
 Pred. No.: 3.06e+04 Length: 24
 Score: 44.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.99% Indels: 0
 DB: 20 Gaps: 0

US-09-375-514-22 (1-205) x AAX26250 (1-24)

QY 140 AspGlyValAsnTrpGlyArg 146

Db 23 GATGGGTGAACCTGGGGAGG 3

RESULT 15

AAV81830/c
 ID AAV81830 standard; DNA; 24 BP.

XX AAV81830;

XX 11-MAR-1999 (first entry)

XX Mouse bcl-2 reverse primer #1.

XX Human; cardiovascular disease; atherosclerosis; ischaemia; restenosis;
 KW reperfusion; hypertension; arterial inflammation; diagnosis; rchd528;
 KW primer; ss.

XX Synthetic.

OS Mus sp.

XX US5849578-A.

XX 15-DEC-1998.

XX 15-MAR-1996; 96US-0616844.

XX 09-FEB-1996; 96US-0599654.

XX 10-FEB-1995; 95US-0386844.

XX 07-JUN-1995; 95US-0488873.

XX 15-MAR-1996; 96US-0616844.

XX (MILL-) MILLENNIUM PHARM INC.

XX Falb DA;

XX WPI; 1999-069743/06.

XX

XX DNA encoding rchd528 polypeptide - associated with cardiovascular
PT disease
XX
PS Example; Column 95; 122pp; English.
XX
XX The present invention describes rchd528 protein. A method has been
CC developed for producing the rchd528 gene product. The present invention
CC also describes methods and compositions for the treatment and diagnosis
CC of cardiovascular diseases, including: atherosclerosis; ischaemia;
CC restenosis; reperfusion; hypertension; and arterial inflammation. The
CC present sequence represents a primer used in an example from the present
CC invention.
XX
SQ Sequence 24 BP; 4 A; 14 C; 1 G; 5 T; 0 other;
Alignment Scores:
Pred. No.: 3.06e+04 Length: 24
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.99% Indels: 0
DB: 20 Gaps: 0
US-09-375-514-22 (1-205) x AAV81830 (1-24)
QY 140 AspGlyValAsnTrpGlyArg 146
DB 23 GATGGGTGAAC TGGGGGAGG 3
RESULT 16
AA88587/C
ID AA88587 standard; DNA; 24 BP.
XX
AC AA88587;
XX
XX 05-FEB-2001 (first entry)
XX
DE PCR primer for mouse bcl-2 gene.
XX
XX Mouse; bcl-2 gene; differential expression; atherosclerosis;
KW cardiovascular disease; diagnosis; therapy; PCR primer; ss.
XX
XX Mus sp.
XX
XX US6124433-A.
XX
XX 26-SEP-2000.
XX
XX 06-OCT-1997; 97US-0944496.
XX
XX 09-FEB-1996; 96US-0599654.
PR 10-FEB-1995; 95US-0386844.
PR 07-JUN-1995; 95US-0485573.
XX
XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX Gimbrone MA, Falb DA;
XX
XX WPI; 2000-611017/58.
XX
XX Novel isolated rchd502 polypeptides, differentially expressed in
PT response to endothelial cell shear stress, used for diagnosis,
PT monitoring clinical trails, and treating cardiovascular diseases such
XX as ischemia -
XX
XX Example 7; Column 9; 123pp; English.
XX
XX This oligonucleotide is a reverse PCR primer for the mouse bcl-2
CC gene. It was used with the forward primer given in AAA88586 in a
CC quantitative RT-PCR analysis of mouse bcl-2 mRNA levels in
CC apoE-deficient mice, a murine model of atherosclerosis. bcl-2

CC mRNAs were shown to be lower in apoE-deficient mice relative to
CC wild-type controls. The invention provides novel human genes (see
CC AAA88576-83) that are differentially expressed in cardiovascular
CC disease states, and which are of diagnostic and therapeutic use.
XX
SQ Sequence 24 BP; 4 A; 14 C; 1 G; 5 T; 0 other;
Alignment Scores:
Pred. No.: 3.06e+04 Length: 24
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.99% Indels: 0
DB: 21 Gaps: 0
US-09-375-514-22 (1-205) x AAA88587 (1-24)
QY 140 AspGlyValAsnTrpGlyArg 146
DB 23 GATGGGTGAAC TGGGGGAGG 3
RESULT 17
AA88580/C
ID AA88580 standard; cDNA; 24 BP.
XX
AC AA88580;
XX
XX 05-MAY-2000 (first entry)
XX
DE Reverse primer for mouse bcl2 amplification.
XX
XX Differentially expressed; cardiovascular disease; atherosclerosis;
KW ischaemia; reperfusion; hypertension; restenosis; arterial inflammation;
KW bcl2; differential display analysis; ss.
XX
XX Mus sp.
XX
XX US6020463-A.
XX
XX 01-FEB-2000.
XX
XX 06-OCT-1997; 97US-0944423.
XX
XX 09-FEB-1996; 96US-0599654.
PR 10-FEB-1995; 95US-0386844.
PR 07-JUN-1995; 95US-0485573.
XX
XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX Gimbrone MA, Falb DA;
XX
XX WPI; 2000-146911/13.
XX
XX Marker proteins for the diagnosis of cardiovascular diseases such as
PT atherosclerosis and hypertension, comprising peptide sequences derived
PT from the rchd523 transmembrane protein -
XX
XX Disclosure; Column 9; 121pp; English.
XX
XX This sequence represents a PCR primer used to amplify the mouse bcl2
CC nucleotide sequence. The primer is used in methods for the
CC identification of the marker proteins and differentially expressed genes
CC of the invention. The invention relates to the rchd523 transmembrane
CC polypeptide (see AAY78506) encoded by cDNA contained in the plasmid
CC pfchd523. The rchd523 protein is differentially expressed in diseased
CC cells compared to healthy cells. The rchd523 protein may be used as a
CC marker protein for the diagnosis of cardiovascular diseases including
CC atherosclerosis, ischaemia, reperfusion, hypertension, restenosis and
CC arterial inflammation. rchd523 peptides may be used as antigens in the
CC production of antibodies specific for rchd523. The anti-rchd523
CC antibodies may then be used in diagnostic assays to quantitate rchd523
CC peptides in samples.

XX SQ Sequence 24 BP; 4 A; 14 C; 1 G; 5 T; 0 other;

Alignment Scores:
Pred. No.: 3.06e+04 Length: 24
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.99% Indels: 0
DB: 21 Gaps: 0

US-09-375-514-22 (1-205) x AAZ89800 (1-24)

OY 140 AspGlyValAsnTrrpGlyArg 146

DB 23 GATGGGTGAACCTGGGGGAGG 3

RESULT 18

AAZ88011/c

ID AAZ88011 standard; DNA; 24 BP.

XX AC AAZ88011;

DT 19-APR-2000 (first entry)

DE Mouse bcl-2 reverse PCR primer SEQ ID NO:11.

KW Cardiovascular disease; diagnosis; atherosclerosis; ischaemia;
KW reperfusion; hypertension; restenosis; arterial inflammation;
KW antiarteriosclerotic; vasotropic; hypotensive; PCR primer; ss.

XX OS Mus sp.

XX US6018025-A.

PD 25-JAN-2000.

PF 06-OCT-1997; 97US-0944868.

PR 09-FEB-1996; 96US-0599654.

PR 10-FEB-1995; 95US-0386844.

PR 07-JUN-1995; 95US-0485573.

XX (MILL-) MILLENIUM PHARM INC.

PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX Falb DA, Gimbrone MA;

DR WPI; 2000-136704/12.

XX Isolated polypeptide for treating and diagnosing cardiovascular

PT disease, such as, atherosclerosis, ischemia/reperfusion, hypertension,

PT restenosis and arterial inflammation -

XX Example; Column 9; 122pp; English.

XX The present invention describes an isolated polypeptide (I) comprising
CC either the amino acid sequence of 1481 residues, given in AAY68447, or
CC an amino acid sequence encoded by the cDNA contained in plasmids
CC pFCHD528A (ATCC 69985), pFCHD528B (ATCC 69986) and pFCHD528C (ATCC
CC 69987). The polypeptide is useful in the treatment and diagnosis of
CC cardiovascular disease, such as, atherosclerosis, ischaemia/reperfusion,
CC hypertension, restenosis and arterial inflammation. AAZ88001 to AAZ88040,
CC and AAY68444 to AAY68457 represent sequences used in the exemplification
CC of the present invention.

XX SQ Sequence 24 BP; 4 A; 14 C; 1 G; 5 T; 0 other;

Alignment Scores:
Pred. No.: 3.06e+04 Length: 24
Score: 44.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

XX Query Match: 3.99% Indels: 0
DB: 21 Gaps: 0

US-09-375-514-22 (1-205) x AAZ88011 (1-24)

OY 140 AspGlyValAsnTrrpGlyArg 146

DB 23 GATGGGTGAACCTGGGGGAGG 3

RESULT 19

AAA73296

ID AAA73296 standard; DNA; 25 BP.

XX AC AAA73296;

DT 06-DEC-2000 (first entry)

DE Bcl-2 specific gene amplification PCR primer #1.

KW STAT; signal transducer and activator of transcription; human; cancer;
KW cell signalling; cytokine; growth factor; oncogenesis; tumour;
KW apoptosis; cytostatic; tumorigenesis; PCR primer; ss.

XX OS Homo sapiens.

XX WO2000044774-A2.

PD 03-AUG-2000.

PF 27-JAN-2000; 2000WO-US01845.

PR 27-JAN-1999; 99US-0117600.

XX (UYSF-) UNIV SOUTH FLORIDA.

XX Jove R, Dalton W, Sebt S, Yu H, Heller R, Jaroszeski M;

PI WPI; 2000-505964/45.

DR Administering antagonists of STAT (signal transducer and activator of
XX transcription) signaling in cells for the treatment of cancers -

XX Example 9; Page 31; 92pp; English.

XX The present invention describes methods for inhibiting the growth of
CC (I), inducing apoptosis in (II), inhibiting tumorigenesis in (III),
CC inhibiting neoplastic transformation in (IV) cancer cells and for
CC enhancing the effectiveness of chemo-(IV) and radiotherapies (VI) for
CC the treatment of cancer. The methods comprise administering an antagonist
CC of STAT (signal transducer and activator of transcription) signalling.
CC The methods may be used for inhibiting the growth of cancer cells (I),
CC inducing apoptosis in cancer cells (II), inhibiting tumorigenesis
CC in cancer cells (III), inhibiting neoplastic transformation in cancer
CC cells (IV) and for enhancing the effectiveness of chemo-(IV) and
CC radiotherapies (VI) for the treatment of cancer. The present sequence
CC represents a specific gene amplification PCR primer for bcl-2, which
CC is used in an example from the present invention.

XX SQ Sequence 25 BP; 3 A; 13 C; 5 G; 4 T; 0 other;

Alignment Scores:
Pred. No.: 3.19e+04 Length: 25
Score: 44.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.99% Indels: 0
DB: 21 Gaps: 0

US-09-375-514-22 (1-205) x AAA73296 (1-25)

OY 102 AspAspPheSerArgTyrArg 109

DB 2 GACGACTTCTCCGCCGCTACGCG 25

RESULT 20
 AAH45305/c
 ID AAH45305 standard; DNA; 27 BP.
 XX
 AC AAH45305;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Human Bcl-2 mutagenic primer oligo-8 for S161A substitution.
 XX
 KW Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200142459-A1.
 XX
 PD 14-JUN-2001.
 XX
 PF 07-DEC-2000; 2000WO-JP08667.
 XX
 PR 09-DEC-1999; 95JP-0350427.
 XX
 PA (HISM) HISAMITSU PHARM CO LTD.
 XX
 PI Shibasaki F, Kuma H;
 XX
 DR WPI; 2001-381681/40.
 XX
 PT New apoptosis inhibitors, useful for treating apoptosis related
 PT disorders -
 XX
 PS Example 1; Page 11; 43pp; Japanese.
 XX
 CC The invention relates to an apoptosis inhibitor comprising the
 CC amino acid sequence of Bcl-2 protein in which at least one serine
 CC residue is substituted by alanine or aspartic acid. The protein has
 CC increased apoptosis inhibitory activity compared with the wild type
 CC Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment
 CC of disorders caused by apoptosis. The present sequence was used to
 CC create a mutant Bcl-2 protein of the invention.
 XX
 SQ Sequence 27 BP; 5 A; 12 C; 5 G; 5 T; 0 other;
 Alignment Scores:
 Pred. No.: 3.46e+04 Length: 27
 Score: 44.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 88.89% Mismatches: 0
 Query Match: 3.99% Indels: 0
 DB: 22 Gaps: 0
 US-09-375-514-22 (1-205) x AAH45305 (1-27)
 QY 157 MetCysValGluSerValAsnArgGlu 165
 Db 27 ATGTGTGTGGAGCGCGTCAACGGGAG 1
 RESULT 21
 AAL46663/c
 ID AAL46663 standard; DNA; 27 BP.
 XX
 AC AAL46663;
 XX
 DT 05-AUG-2002 (first entry)
 XX
 DE Human bcl-2 mRNA probe.
 XX
 KW Human; bcl-2; cancer detection; disseminated cancer cell; cytostatic;
 KW probe; ss.
 XX
 OS Homo sapiens.

XX WO200237113-A2.
 PN 10-MAY-2002.
 XX
 PD 05-NOV-2001; 2001WO-EPI2786.
 XX
 PF 03-NOV-2000; 2000DE-1054635.
 XX
 PR 03-NOV-2000; 2000US-245854P.
 XX
 PA (GIES/) GIESING M.
 XX
 PI Giesing M, Grill H, Boeckmann B, Suchy B;
 XX
 DR WPI; 2002-426739/45.
 XX
 PT Clinically validating target from disseminated cancer cells by
 PT determining whether status of target determined in cancer cells of
 PT individuals correlates with cancer-related information about clinical
 PT status of individuals -
 XX
 PS Example 3; Page 55; 57pp; English.
 XX
 CC The present invention relates to a method for the clinical validation of
 CC a target from disseminated cancer cells, characterised in that for a
 CC population of individuals it is determined whether a status of the target
 CC determined in disseminated cancer cells of the individuals correlates
 CC with at least one cancer-related information about the clinical status of
 CC the individuals. The method is useful for clinically validating target
 CC from disseminated cancer cells. The present sequence is a probe used
 CC to demonstrate the method of the invention.
 XX
 SQ Sequence 27 BP; 6 A; 7 C; 7 G; 7 T; 0 other;
 Alignment Scores:
 Pred. No.: 3.46e+04 Length: 27
 Score: 44.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.99% Indels: 0
 DB: 24 Gaps: 0
 US-09-375-514-22 (1-205) x AAL46663 (1-27)
 QY 172 AsnIleAlaLeuTrpMetThrGlu 179
 Db 25 AACATCGCCCTGTGGATGACTGAG 2
 RESULT 22
 ABR66508/c
 ID ABR66508 standard; DNA; 25 BP.
 XX
 AC ABR66508;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human gene specific PCR primer #596.
 XX
 KW Primer; ss; DNA microarray; differential expression analysis; human.
 XX
 OS Homo sapiens.
 XX
 PN US6352829-B1.
 XX
 PD 05-MAR-2002.
 XX
 PF 05-JAN-1999; 99US-0225928.
 XX
 PR 21-MAY-1997; 97US-0859998.
 XX
 PA (CLON-) CLONTECH LAB INC.
 XX
 PI Chenchik A, Jokhadze G, Bibilashvilli R;

XX WPI; 2002-314699/35.
XX Producing sub-population of labeled nucleic acids, useful for analysing
PT differences in RNA profiles between several different physiological
PT sources, using set of distinct gene specific primers -
XX
XX Example 3; SEQ ID No 596; 11pp; English.
XX
XX The invention relates to producing a sub-population of labeled nucleic
CC acids (NAs) comprising contacting a NA sample from a physiological
CC source, with a pool of 50 distinct gene specific primers under suitable
CC conditions to enzymatically generate sub-population of NAs, where
CC each gene specific primer has a sequence complementary to a distinct
CC mRNA, and each labeled NA is generated using a single gene specific
CC primer. The method is useful for producing a sub-population of labeled
CC NAs which is useful for analysing the differences in the RNA profiles
CC between several different physiological sources, where the method
CC comprises producing subpopulation of labeled NAs for the different
CC physiological sources, comprising the populations for each physiological
CC source to identify differences in the population, where the comparison
CC is preferably performed by hybridising the labeled NAs for each of the
CC distinct physiological sources to an array of probe NAs stably
CC associated with the surface of a substrate to produce a hybridisation
CC pattern for each of the sources, and comparing the patterns for each of
CC the sources, where differential gene expression assays are
CC utilised in differential expression analysis of diseased a normal
CC tissue e.g. neoplastic a normal tissue, or different tissue or
CC sub tissue types. The present sequence is a human gene specific PCR
CC primer used in the method of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from USPTO at
CC <http://wipo.seqdata.uspto.gov/sequence.html?DocID=6352829B1>.
XX
XX Sequence 25 BP; 5 A; 11 C; 4 G; 5 T; 0 other;

Alignment Scores:
Pred. No.: 4.34e+04 Length: 25
Score: 42.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 3.80% Indels: 0
DB: 24 Gaps: 0

US-09-375-514-22 (1-205) x ABK66508 (1-25)

QY 189 IleGlnAspAsnGlyGlyTrpVal 196
DB 24 ATCCAAGACCCAGGGTGGTGGGTG 1

RESULT 23

AAH45298/C
ID AAH45298 standard; DNA; 27 BP.

XX
XX AAH45298;

XX 10-SEP-2001 (first entry)

XX Human Bcl-2 mutagenic primer oligo-1 for S24A substitution.

XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.

XX Homo sapiens.

OS Synthetic.

XX WO200142459-A1.

XX 14-JUN-2001.

XX 07-DEC-2000; 2000WO-JP08667.

XX 09-DEC-1999; 99JP-0350427.

XX
PA (HISM) HISAMITSU PHARM CO LTD.
XX
PI Shibazaki F, Kuma H;
XX WPI; 2001-381681/40.
XX
XX New apoptosis inhibitors, useful for treating apoptosis related
PT disorders -
XX
XX Example 1; Page 10; 43pp; Japanese.
XX
XX The invention relates to an apoptosis inhibitor comprising the
CC amino acid sequence of Bcl-2 protein in which at least one serine
CC residue is substituted by alanine or aspartic acid. The protein has
CC increased apoptosis inhibitory activity compared with the wild type
CC Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment
CC of disorders caused by apoptosis. The present sequence was used to
CC create a mutant Bcl-2 protein of the invention.
XX
XX Sequence 27 BP; 5 A; 7 C; 8 G; 7 T; 0 other;

Alignment Scores:
Pred. No.: 4.67e+04 Length: 27
Score: 42.00 Matches: 7
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 1
Query Match: 3.80% Indels: 0
DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x AAH45298 (1-27)

QY 20 HisTyrLysLeuSergGlnArgGlyTyr 28

DB 27 CATTATAAGCTGGCGAGACCCGGCTAC 1

RESULT 24

AAH45302/C

ID AAH45302 standard; DNA; 27 BP.

XX
XX AAH45302;

XX 10-SEP-2001 (first entry)

XX Human Bcl-2 mutagenic primer oligo-5 for S116A substitution.

XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.

XX Homo sapiens.

OS Synthetic.

XX WO200142459-A1.

XX 14-JUN-2001.

XX 07-DEC-2000; 2000WO-JP08667.

XX 09-DEC-1999; 99JP-0350427.

XX (HISM) HISAMITSU PHARM CO LTD.

XX Shibazaki F, Kuma H;

XX WPI; 2001-381681/40.

XX New apoptosis inhibitors, useful for treating apoptosis related
PT disorders -

XX Example 1; Page 11; 43pp; Japanese.

XX The invention relates to an apoptosis inhibitor comprising the
CC amino acid sequence of Bcl-2 protein in which at least one serine
CC residue is substituted by alanine or aspartic acid. The protein has

CC increased apoptosis inhibitory activity compared with the wild type
 CC Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment
 CC of disorders caused by apoptosis. The present sequence was used to
 CC create a mutant Bcl-2 protein of the invention.

SQ Sequence 27 BP; 4 A; 8 C; 10 G; 5 T; 0 other;

Alignment Scores:
 Pred. No.: 4.67e+04 Length: 27
 Score: 42.00 Matches: 8
 Percent Similarity: 100.00% Conservatives: 1
 Best Local Similarity: 88.89% Mismatches: 0
 Query Match: 3.80% Indels: 0
 DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x AAH45302 (1-27)

Qy 112 PheAlaGluMetSerSerGlnLeuHis 120
 ID AAT42430 standard; DNA; 39 BP.
 XX AC AAT42430;
 XX AC AAT42430;
 DT 29-JUL-1997 (first entry)
 XX GD domain region for Bak encoding DNA, amino acid residues 82-94.
 DE GD domain region for Bak encoding DNA, amino acid residues 82-94.
 KW Apoptosis; follicular lymphoma; tumour; p53; antibody; ss.
 XX Synthetic.
 OS Synthetic.
 XX WO9635951-A1.
 PN WO9635951-A1.
 XX 14-NOV-1996.
 PD 14-NOV-1996.
 PF 06-MAY-1996; 96WO-US06122.
 PR 12-MAY-1995; 95US-0440391.
 XX (IMMU-) IMMUNOGEN INC.
 PA Chittenden TD, Lutz RJ;
 PI WPI; 1996-518805/51.
 XX P-PSDB; AA06293.
 DR Peptide(s) comprising GD domains - have similar activities to wild
 XX type Bak, and cause cellular apoptosis for treatment of viral
 PT infection
 PS Claim 6; Page 45; 69pp; English.
 XX The term GD domain refers to a protein domain first identified in
 CC Bak and shown to be essential for the interaction of Bak with Bcl-x(L)
 CC and for Bak's cell killing function; and to peptides and/or molecules
 CC capable of mimicking its structure and/or function. The present sequence
 CC encodes a GD domain corresponding to amino acid residues 82-94 of Bak.
 CC An antibody raised against a GD domain may be used to screen a cDNA
 CC expression library for clones comprising cDNA inserts encoding
 CC immunoreactive proteins. Truncated GD domain peptides have been
 CC shown to maintain the protein binding and cell killing function
 CC exhibited by wild type Bak. These molecules may induce apoptosis in
 CC tumour cell. These peptides act independently of p3 status. Bak or
 CC GD domain mimetics that inhibit Bcl-2 may be selectively toxic to
 CC certain tumours, e.g. follicular lymphoma, which depend on high levels
 CC of Bcl-2 for their continued growth and survival. GD domain mimetics
 CC may also be used for combating viral infections by causing apoptosis
 CC of infected cells.

RESULT 25

AAT42430
 ID AAT42430 standard; DNA; 39 BP.
 XX AC AAT42430;
 XX AC AAT42430;
 DT 29-JUL-1997 (first entry)
 XX GD domain region for Bak encoding DNA, amino acid residues 82-94.
 DE GD domain region for Bak encoding DNA, amino acid residues 82-94.
 KW Apoptosis; follicular lymphoma; tumour; p53; antibody; ss.
 XX Synthetic.
 OS Synthetic.
 XX WO9635951-A1.
 PN WO9635951-A1.
 XX 14-NOV-1996.
 PD 14-NOV-1996.
 PF 06-MAY-1996; 96WO-US06122.
 PR 12-MAY-1995; 95US-0440391.
 XX (IMMU-) IMMUNOGEN INC.
 PA Chittenden TD, Lutz RJ;
 PI WPI; 1996-518805/51.
 XX P-PSDB; AA06293.
 DR Peptide(s) comprising GD domains - have similar activities to wild
 XX type Bak, and cause cellular apoptosis for treatment of viral
 PT infection
 PS Claim 6; Page 45; 69pp; English.
 XX The term GD domain refers to a protein domain first identified in
 CC Bak and shown to be essential for the interaction of Bak with Bcl-x(L)
 CC and for Bak's cell killing function; and to peptides and/or molecules
 CC capable of mimicking its structure and/or function. The present sequence
 CC encodes a GD domain corresponding to amino acid residues 82-94 of Bak.
 CC An antibody raised against a GD domain may be used to screen a cDNA
 CC expression library for clones comprising cDNA inserts encoding
 CC immunoreactive proteins. Truncated GD domain peptides have been
 CC shown to maintain the protein binding and cell killing function
 CC exhibited by wild type Bak. These molecules may induce apoptosis in
 CC tumour cell. These peptides act independently of p3 status. Bak or
 CC GD domain mimetics that inhibit Bcl-2 may be selectively toxic to
 CC certain tumours, e.g. follicular lymphoma, which depend on high levels
 CC of Bcl-2 for their continued growth and survival. GD domain mimetics
 CC may also be used for combating viral infections by causing apoptosis
 CC of infected cells.

SQ Sequence 39 BP; 11 A; 11 C; 11 G; 6 T; 0 other;

Alignment Scores:
 Pred. No.: 6.81e+04 Length: 39
 Score: 42.00 Matches: 7
 Percent Similarity: 75.00% Conservatives: 2
 Best Local Similarity: 58.33% Mismatches: 3
 Query Match: 3.80% Indels: 0
 DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x AAT42430 (1-39)

Qy 101 GlyAspAspPheSerArgArgTyrArgGlyAspPhe 112
 ID AAT42430 standard; DNA; 39 BP.
 XX AC AAT42430;
 XX AC AAT42430;
 DT 05-JUN-2002 (first entry)
 XX DNA encoding Bak GD domain region #1 for modulating apoptosis.
 DE DNA encoding Bak GD domain region #1 for modulating apoptosis.
 KW GD domain; apoptosis; interaction with Bcl-XL; cell killing function;
 KW bak; cell death regulatory molecule; autoimmune disease; cancer; ds.
 XX Unidentified.
 OS Unidentified.
 XX Key Location/Qualifiers
 FH 1..39
 FT CDS
 FT /*tag= a
 FT /partial
 FT /product= "Bak GD domain region #1"
 FT /note= "This sequence lacks both start and stop codons"

RESULT 26

ABK11179
 ID ABK11179 standard; DNA; 39 BP.
 XX AC ABK11179;
 XX AC ABK11179;
 DT 05-JUN-2002 (first entry)
 XX DNA encoding Bak GD domain region #1 for modulating apoptosis.
 DE DNA encoding Bak GD domain region #1 for modulating apoptosis.
 KW GD domain; apoptosis; interaction with Bcl-XL; cell killing function;
 KW bak; cell death regulatory molecule; autoimmune disease; cancer; ds.
 XX Unidentified.
 OS Unidentified.
 XX Key Location/Qualifiers
 FH 1..39
 FT CDS
 FT /*tag= a
 FT /partial
 FT /product= "Bak GD domain region #1"
 FT /note= "This sequence lacks both start and stop codons"

US6221615-B1.

24-APR-2001.

25-JAN-1999; 99US-0236385.

12-MAY-1995; 95US-0440391.

08-AUG-1997; 97US-0908597.

(APOP-) APOPTOSIS TECHNOLOGY INC.

Chittenden TD, Lutz RJ;

WPI; 2002-234950/29.

P-PSDB; AAU77876.

Identifying agents (e.g. modulators of apoptosis) capable of modulating
 GD domain mediated heterodimerisation or homodimerisation comprises
 carrying out a heterodimerisation or homodimerisation assay
 Disclosure; Fig 8B; 37pp; English.
 The present invention relates to novel peptides, designated GD domains,
 which are capable of modulating apoptosis. The GD domains are essential
 for Bak's interaction with Bcl-XL, and to Bak's cell killing function.
 The GD domains mediate key protein/protein interactions with multiple
 cell death regulatory molecules. Also described are methods of
 identifying agonists or antagonists of GD domains. The methods are
 useful for identifying agents capable of modulating GD domain mediated
 heterodimerisation or homodimerisation. The methods are particularly
 useful in drug screening and design, e.g. for identifying agents for
 treating autoimmune disease or cancer, or for identifying modulators
 of apoptosis. The present DNA sequence encodes a GD domain region.

SQ Sequence 39 BP; 11 A; 11 C; 11 G; 6 T; 0 other;

Alignment Scores:
 Pred. No.: 6.81e+04 Length: 39
 Score: 42.00 Matches: 7
 Percent Similarity: 75.00% Conservative: 2
 Best Local Similarity: 58.33% Mismatches: 3
 Query Match: 3.80% Indels: 0
 DB: 24 Gaps: 0

US-09-375-514-22 (1-205) x ABK11179 (1-39)

Qy 101 GlyAspPheSerArgArgTyrArgGlyAspPhe 112
 ||||| :|||
 Db 1 GGGGACGACATCAACCGACGCTATGACTCAGAGTTC 36

RESULT 27

AAH45293/c

ID AAH45299 standard; DNA; 27 BP.

XX

XX

XX

DT 10-SEP-2001 (first entry)

XX

DE Human Bcl-2 mutagenic primer oligo-2 for S24D substitution.

XX

KW Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.

XX

OS Homo sapiens.

OS Synthetic.

PN WO200142459-A1.

XX

PD 14-JUN-2001.

XX

PF 07-DEC-2000; 2000WO-JP08667.

XX

PR 09-DEC-1999; 99JP-0350427.

XX

PA (HISM) HISAMITSU PHARM CO LTD.

XX

PI Shibazaki F., Kuma H;

XX

DR WPI; 2001-381681/40.

XX

PT New apoptosis inhibitors, useful for treating apoptosis related disorders

XX

PS Example 1; Page 10; 43pp; Japanese.

XX

CC The invention relates to an apoptosis inhibitor comprising the amino acid sequence of Bcl-2 protein in which at least one serine residue is substituted by alanine or aspartic acid. The protein has increased apoptosis inhibitory activity compared with the wild type Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment of disorders caused by apoptosis. The present sequence was used to create a mutant Bcl-2 protein of the invention.

XX

SQ Sequence 27 BP; 5 A; 6 C; 8 G; 8 T; 0 other;

Alignment Scores:

Pred. No.: 5.44e+04 Length: 27

Score: 41.00 Matches: 7

Percent Similarity: 77.78% Conservative: 0

Best Local Similarity: 77.78% Mismatches: 2

Query Match: 3.71% Indels: 0

DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x AAH45299 (1-27)

Qy 20 HistTrpLysLeuSerGlnArgGlyTyr 28

||||| ||| |||||

Db 27 CATTATAAGCTGGACACGACCGGCTAC 1

RESULT 28

AAH45306/c

ID AAH45306 standard; DNA; 27 BP.

XX

AC AAH45306;

XX

DT 10-SEP-2001 (first entry)

XX

DE Human Bcl-2 mutagenic primer oligo-9 for S161D substitution.

XX

KW Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.

XX

OS Homo sapiens.

OS Synthetic.

PN WO200142459-A1.

XX

PD 14-JUN-2001.

XX

PF 07-DEC-2000; 2000WO-JP08667.

XX

PR 09-DEC-1999; 99JP-0350427.

XX

PA (HISM) HISAMITSU PHARM CO LTD.

XX

PI Shibazaki F., Kuma H;

XX

DR WPI; 2001-381681/40.

XX

PT New apoptosis inhibitors, useful for treating apoptosis related disorders

XX

PS Example 1; Page 11; 43pp; Japanese.

XX

CC The invention relates to an apoptosis inhibitor comprising the amino acid sequence of Bcl-2 protein in which at least one serine residue is substituted by alanine or aspartic acid. The protein has increased apoptosis inhibitory activity compared with the wild type Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment of disorders caused by apoptosis. The present sequence was used to create a mutant Bcl-2 protein of the invention.

XX

SQ Sequence 27 BP; 6 A; 12 C; 4 G; 5 T; 0 other;

Alignment Scores:

Pred. No.: 5.44e+04 Length: 27

Score: 41.00 Matches: 8

Percent Similarity: 88.89% Conservative: 0

Best Local Similarity: 88.89% Mismatches: 1

Query Match: 3.71% Indels: 0

DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x AAH45306 (1-27)

Qy 157 MetCysValGluSerValAsnArgGlu 165

||||| ||||| |||||

Db 27 ATGTGTGTGGAGTCTCAACCGGGAG 1

RESULT 29

AAH45306/c

ID AAH45306 standard; DNA; 31 BP.

XX

AC AAH45306;

XX

DT 22-APR-1998 (first entry)

XX

DE Mouse bcl-w gene PCR primer 2.

XX

KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer; diagnosis; degenerative disease; PCR primer; ss.

XX

OS Synthetic.

OS Mus sp.

XX Key Location/Qualifiers
 FT modified_base 14
 FT /*tag= a
 FT /mod_base= i
 FT /note= "inosine"
 FT modified_base 17
 FT /*tag= b
 FT /mod_base= i
 FT /note= "inosine"
 FT modified_base 20
 FT /*tag= c
 FT /mod_base= i
 FT /note= "inosine"

W09735971-A1.

02-OCT-1997.

27-MAR-1997; 97WO-AU00199.

27-MAR-1996; 96AU-0008965.

(AMRA-) AMRAD OPERATIONS PTY LTD.

Adams JM, Cory S, Gibson LM, Holmgren SP;

WPI; 1997-489635/45.

Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases

Example 1; Page 30; 86pp; English.

AAT96580 and AAT96579 are PCR primers used to amplify a novel gene, bcl-w, a member of the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators.

Sequence 31 BP; 5 A; 10 C; 5 G; 7 T; 4 other;

Alignment Scores:
 Pred. No.: 6.27e+04 Length: 31
 Score: 41.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 3.71% Indels: 0
 DB: 18 Gaps: 0

US-09-375-514-22 (1-205) x AAT96580 (1-31)

QY 188 TrpIleGlnAspAsnGlyClyTrp 195

Db 31 TGGATCCCAAGANMANGGCGCTGG 8

RESULT 30

AAT92245/C

ID AAT92245 standard; DNA; 36 BP.

XX AC AAT92245;

XX DT 19-JAN-1998 (first entry)

XX DE Mercuric ion reductase merA PCR mutagenesis primer 3'A.

XX

KW Metal ion resistance; mercuric ion reductase; merA; mercury;
 KW toxic heavy metal; transgenic plant; mutagenic; bacterial;
 KW transposon; Tn21; PCR; ss.

XX Synthetic.
 OS Transposon Tn21.

XX US5668294-A.

XX 16-SEP-1997.

XX 21-APR-1995; 95US-0427097.

XX 21-APR-1995; 95US-0427097.

XX (UYGE-) UNIV GEORGIA RES FOUND INC.

XX Meagher RB, Summers AO;

XX WPI; 1997-470112/43.

XX DNA encoding mercuric ion reductase in plant-expressible form - for
 XX producing transgenic plants resistant to toxic heavy metals

XX Example 1; Column 45; 52pp; English.

XX The present sequence represents a PCR mutagenesis primer used to
 CC mutagenise the merA coding sequence derived from transposon Tn21, to
 CC adapt it for plant expressibility. The nucleic acid molecule produced
 CC is useful for producing transgenic plants that are resistant to toxic
 CC heavy metals (especially mercury) and so can be used to remediate and/or
 CC revegetate contaminated areas. The bacterial merA gene is derived from
 CC the transposon Tn21, which was originally isolated from the
 CC Incompatibility Group IncFII resistance plasmid NR1.

XX Sequence 36 BP; 8 A; 13 C; 9 G; 6 T; 0 other;

Alignment Scores:
 Pred. No.: 7.31e+04 Length: 36
 Score: 41.00 Matches: 8
 Percent Similarity: 88.89% Conservative: 0
 Best Local Similarity: 88.89% Mismatches: 1
 Query Match: 3.71% Indels: 0
 DB: 18 Gaps: 0

US-09-375-514-22 (1-205) x AAT92245 (1-36)

QY 75 ProAlaAlaProGlyAlaAlaAlaGly 83

Db 35 CCTGCTGCGCGGCTGAGGCTGCAGGA 9

RESULT 31

AAZ28595/C

ID AAZ28595 standard; DNA; 36 BP.

XX AC AAZ28595;

XX 24-DEC-1999 (first entry)

XX Primer 3'N for Tn21 merA gene.

XX Organometal; resistance; transcription; translation; regulation; merA;
 KW transposon; Tn21; merB; mercuric ion reductase; organomercury lyase; ss;
 KW transgenic plant; detoxification; metal compound; soil; sediment; primer;
 KW aquatic environment; bioremediation; contamination; PCR; amplification.

XX Synthetic.

XX Transposon Tn21.

XX US5965796-A.

XX 12-OCT-1999.

XX

PR 23-OCT-1995; 95US-0535168.
 PR 19-MAR-1996; 96US-0013688.
 PR 25-MAR-1996; 96US-0014007.
 PR 17-APR-1996; 96US-0015714.
 PA (ARON-) ARONEX PHARM INC.
 XX
 XX Pennewald S, Hogan ME, Mazumder A, Ojwang JO, Pommier Y;
 PI Rando RF, Zengdegi JG;
 XX
 XX WPI; 1997-132569/12.

XX Oligo:nucleotide(s) capable of forming guanosine tetrads - inhibit
 PT viral enzyme responsible for integrating viral nucleic acid into the
 PT host genome
 XX

PS Claim 3; Page 141; 245pp; English.

XX AAT51619-T51698 are oligonucleotides used to inhibit the production
 CC of viruses within a host cell. The oligonucleotides may form guanosine
 CC tetrads (structures formed of eight hydrogen bonds by coordination of
 CC the four oxygen atoms of guanine with alkali cations believed to bind
 CC to the centre of a quadruplex, and by strong stacking interactions) and
 CC are used to prevent the integration of viral nucleic acid into a host
 CC genome. The oligonucleotides inhibit functioning of the integrase enzyme
 CC and hence prevent viral infection. Viral infections that may be treated
 CC include human immunodeficiency virus (HIV), Epstein Barr virus (EBV),
 CC herpes simplex virus (HSV), human papilloma virus (HPV), adenovirus,
 CC respiratory syncytial virus (RSV), cytomegalovirus (CMV) and hepatitis
 CC B virus (HBV), especially HIV-1 infection.
 XX

SQ Sequence 38 BP; 0 A; 0 C; 29 G; 9 T; 0 other;

Alignment Scores: Pred. No.: 7.72e+04 Length: 38
 Score: 41.00 Matches: 8
 Percent Similarity: 50.00% Conservative: 0
 Best Local Similarity: 50.00% Mismatches: 2
 Query Match: 3.71% Indels: 6
 DB: 18 Gaps: 1

US-09-375-514-22 (1-205) x AAT51620 (1-38)

Qy 44 ProAlaProGlyIlePheSerSerGlnProGlyHisThrProHisPro 59

Db 32 CCCACCCCA-----CCCCCCCCACACCCACACCC 3

RESULT 36

AA79211/c
 ID AAX79211 standard; DNA; 38 BP.

XX AAX79211;

DT 31-AUG-1999 (first entry)

XX Oligonucleotide #4 forms an intramolecular stacked tetrad structure.

XX Column: box; stacked tetrad; inhibition; replication; pathophysiological;
 KW herpes simplex virus; HSV; human papilloma virus; Epstein Barr virus;
 KW HPV; EBV; HIV; human immunodeficiency virus; adenovirus; RSV; HBV; HCMV;
 KW respiratory syncytial virus; hepatitis B virus; human cytomegalovirus;
 KW human T-cell leukaemia virus; HTLV; ss.

XX Synthetic.

XX Key Location/Qualifiers
 FT modified_site 1.38
 FT /tag= a

FT /note= "optionally contains phosphodiester
 FT internucleotide linkages"

FT misc_structure 1.38
 FT /tag= b

FT /note= "forms intramolecular stacked tetrad or 3D

columnar box structure"

WO9833807-A1.

06-AUG-1998.

03-FEB-1998; 98WO-US01974.

09-DEC-1997; 97US-0987574.

04-FEB-1997; 97US-0037374.

(ARON-) ARONEX PHARM INC.

Cossum PA, Hogan ME, Ojwang JO, Rando RF, Wallace TL;

WPI; 1998-446809/38.

XX New guanosine-rich tetrad forming oligonucleotide(s) - used for
 PT inhibiting virus replication for treating e.g. herpes simplex,
 PT papilloma, HIV, adenovirus or hepatitis B virus infection
 XX
 PS Disclosure; Page 135; 140pp; English.

XX Sequences AAX79210-X79275 represent oligonucleotides (ON) which are able
 CC to form a columnar box or "stacked tetrad" structure by intramolecular
 CC internucleotide binding. The ONs are used to inhibit the replication
 CC of viruses. They are able to suppress virus production for prolonged
 CC periods after an initial short treatment regimen. They can be used for
 CC treating pathophysiological states caused by viruses such as herpes
 CC simplex virus, human papilloma virus, Epstein Barr virus, HIV,
 CC adenovirus, respiratory syncytial virus, hepatitis B virus, human
 CC cytomegalovirus and HTLV I and II.

SQ Sequence 38 BP; 0 A; 0 C; 29 G; 9 T; 0 other;

Alignment Scores: Pred. No.: 7.72e+04 Length: 38
 Score: 41.00 Matches: 8
 Percent Similarity: 50.00% Conservative: 0
 Best Local Similarity: 50.00% Mismatches: 2
 Query Match: 3.71% Indels: 6
 DB: 19 Gaps: 1

US-09-375-514-22 (1-205) x AAX79211 (1-38)

Qy 44 ProAlaProGlyIlePheSerSerGlnProGlyHisThrProHisPro 59

Db 32 CCCACCCCA-----CCCCCCCCACACCCACACCC 3

RESULT 37

AAQ95496/c

ID AAQ95496 standard; DNA; 39 BP.

XX AAQ95496;

DT 21-NOV-1995 (first entry)

XX Cdn primer Bclx 2-39.

XX Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
 KW shock; lymphoma; eczema; primer; polymerase chain reaction; PCR;
 KW ss.

XX Synthetic.

XX Key Location/Qualifiers
 FT modified_base 19
 FT /tag= a

FT /mod_base= i
 FT modified_base 22
 FT /tag= b

FT /mod_base= i

```

FT misc_difference 25
FT /*tag= c
FT /*note= "base n at position 25 is not identified"
FT misc_difference 28
FT /*tag= d
FT /*note= "base n at position 28 is not identified"
XX
PN WO9515084-A.
XX
XX 08-JUN-1995.
XX
XX 30-NOV-1994; 94WO-US13930.
XX
XX 07-OCT-1994; 94US-0320157.
XX 30-NOV-1993; 93US-0160067.
XX
XX (LXRB-) LXR BIOTECHNOLOGY INC.
XX
XX Barr PJ, Kiefer MC;
XX
XX WPI; 1995-215106/28.
XX
XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
XX related vectors, transformed cells, proteins and antibodies, useful
XX or diagnosis and treatment e.g. of HIV infection, reperfusion injury
XX etc.
XX
XX Disclosure; Fig.1; 6pp; English.
XX
XX In order to identify new Bcl-2 family members, degenerate PCR
XX primers (AAQ95495-96) based on sequences in these regions were used
XX in the amplification of human heart and B lymphoblastoid cell
XX line WI-L2 cDNA. Cdn-1 cDNA (AAQ95492) was obt'd.
XX
XX Sequence 39 BP; 7 A; 12 C; 5 G; 9 T; 6 other;
XX
XX Alignment Scores:
XX Pred. No.: 7.93e+04 Length: 39
XX Score: 41.00 Matches: 6
XX Percent Similarity: 75.00% Conservative: 0
XX Best Local Similarity: 75.00% Mismatches: 2
XX Query Match: 3.71% Indels: 0
XX DB: 16 Gaps: 0
XX
XX US-09-375-514-22 (1-205) x AAQ95496 (1-39)
XX
XX QY 188 TptleGlnAspAnGlyGlyTtp 195
XX ||||||| |||||||
XX Db 39 TGGATCARGCANGCANGGNTGG 16
XX
XX RESULT 38
XX ABK52487/c
XX ID ABK52487 standard; DNA; 24 BP.
XX
XX AC ABK52487;
XX
XX XX
XX DT 14-AUG-2002 (first entry)
XX
XX XX Fluorescent probe for DNA encoding human bcl-2.
XX
XX DE Human; detection of early stage allergic disease; atopic dermatitis;
XX KW antiallergic; eosinocyte; eosinophil; bcl-2; probe; ss.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1
XX /*tag= a
XX /*note= "OTHER= labelled with FAM
XX (6-carboxy-fluorescein)"
XX modified_base 24
XX /*tag= b

```


CC See also AAV13426-28 and AAR13939.

XX Sequence 40 BP; 11 A; 14 C; 8 G; 7 T; 0 other;

Alignment Scores:
Pred. No.: 9.47e+04 Length: 40
Score: 40.00 Matches: 6
Percent Similarity: 85.71% Conservative: 0
Best Local Similarity: 85.71% Mismatches: 1
Query Match: 3.62% Indels: 0
DB: 12 Gaps: 0

US-09-375-514-22 (1-205) x AAV13427 (1-40)

QY 53 ProGlyHisThrProHisPro 59

DB 1 CCAGGACGACGCCACATCCA 21

RESULT 42

AAV74159

ID AAV74159 standard; DNA; 40 BP.

XX AC AAV74159;

DT 12-APR-1999 (first entry)

DE Human mature von Willebrand Factor DNA probe.

XX von Willebrand Factor; vWF; human; GPIb binding domain;
KW antiagregant; platelet aggregation; cerebrovascular disorder;
KW cardiovascular disorder; myocardial infarction; angina;
KW thrombolytic; platelet adhesion; therapy; probe; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN US5849702-A.

XX PD 15-DEC-1998.

XX PF 05-JUN-1995; 95US-0464962.

XX PR 03-SEP-1991; 91US-0753815.

XX PR 02-MAR-1990; 90US-0487767.

XX PR 01-MAR-1991; 91WO-US01416.

XX PR 22-JUN-1993; 93US-0080690.

XX PR 30-NOV-1994; 94US-0347594.

XX PR 05-JUN-1995; 95US-0464962.

XX PA (BIOT-) BIO-TECHNOLOGY GENERAL CORP.

XX PI Garfinkel L, Richter T;

XX DR WPI; 1999-069781/06.

XX PT Composition for inhibiting blood platelet aggregation - containing

XX PS polypeptide comprising von Willebrand factor GPIb binding domain

XX Example 1; Column 12; 50pp; English.

XX This synthetic oligonucleotide corresponds to nucleotides
CC flanking the 3' end of the human von Willebrand Factor (vWF) GPIb
CC binding domain coding region. It was used as a probe for the
CC detection of vWF sequences in a human endothelial cell cDNA
CC library. A GPIb binding domain 5' probe was also used (see
CC AAV74158). A series of vWF cDNA clones covering the entire GPIb
CC binding domain (see AAV74157) were identified and isolated. The
CC invention provides non-glycosylated, biologically active
CC polypeptides (see AAV90119-20) which comprise the vWF GPIb binding
CC domain. These are used in claimed methods for treating and
CC preventing cerebrovascular and cardiovascular disorders, and for
CC inhibiting platelet aggregation.

XX

SQ Sequence 40 BP; 11 A; 14 C; 8 G; 7 T; 0 other;

Alignment Scores:
Pred. No.: 9.47e+04 Length: 40
Score: 40.00 Matches: 6
Percent Similarity: 85.71% Conservative: 0
Best Local Similarity: 85.71% Mismatches: 1
Query Match: 3.62% Indels: 0
DB: 20 Gaps: 0

US-09-375-514-22 (1-205) x AAV74159 (1-40)

QY 53 ProGlyHisThrProHisPro 59

DB 1 CCAGGACGACGCCACATCCA 21

RESULT 43

AAV08903

ID AAV08903 standard; DNA; 40 BP.

XX AC AAV08903;

DT 26-FEB-1999 (first entry)

DE Probe for Von Willebrand factor coding sequence.

XX Von Willebrand factor; GPIb binding domain; inhibitor; re-occlusion;
KW platelet aggregation; cerebrovascular disorder; cardiovascular disorder;
KW angioplasty; thrombi-containing platelet-rich aggregate; thrombosis;
KW therapy; probe; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN US5849536-A.

XX PD 15-DEC-1998.

XX PF 30-NOV-1994; 94US-0347594.

XX PR 01-MAR-1991; 91WO-US01416.

XX PR 02-MAR-1990; 90US-0487767.

XX PR 03-SEP-1991; 91US-0753815.

XX PR 22-JUN-1993; 93US-0080690.

XX PR 30-NOV-1994; 94US-0347594.

XX PA (BIOT-) BIO-TECHNOLOGY GENERAL CORP.

XX PI Garfinkel L, Richter T;

XX DR WPI; 1999-069733/06.

XX PT Polypeptide comprising von Willebrand factor GPIb binding domain -
XX PS useful as platelet aggregation inhibitor

XX Example 1; Column 13-14; 62pp; English.

XX This sequence represents a probe for DNA encoding the protein of the
CC invention. The protein of the invention is the GPIb binding domain of the
CC von Willebrand factor. The protein is used for inhibiting platelet
CC aggregation, especially for treating cerebrovascular disorders. It is
CC also used for treating cardiovascular disorders, especially acute
CC myocardial infarction or angina. The protein is also used for inhibiting
CC platelet aggregation before, during or after angioplasty, thrombolytic
CC treatment or coronary bypass surgery, for maintaining blood vessel
CC patency before, during or after coronary bypass surgery. It can also be
CC used for inhibiting thrombosis, optionally associated with an
CC inflammatory response, for inhibiting platelet adhesion to damaged
CC vascular surfaces, for preventing platelet adhesion to prosthetic
CC materials or devices, for inhibiting re-occlusion after angioplasty or
CC thrombolysis, or for thrombolytic treatment of thrombi-containing
CC platelet-rich aggregates.

SQ Sequence 40 BP; 11 A; 14 C; 8 G; 7 T; 0 other;

Alignment Scores:
Pred. No.: 9.47e+04 Length: 40
Score: 40.00 Matches: 6
Percent Similarity: 85.71% Conservatives: 0
Best Local Similarity: 85.71% Mismatches: 1
Query Match: 3.62% Indels: 0
DB: 20 Gaps: 0

US-09-375-514-22 (1-205) x AAV08903 (1-40)

QY 53 ProGlyHisThrProHisPro 59

DB 1 CCAGGACGAGCCACATCCA 21

RESULT 44

AAZ56179

ID AAZ56179 standard; DNA; 40 BP.

AC AAZ56179;

XX

XX

DT 27-MAR-2000 (first entry)

XX Probe for human von Willebrand Factor (vWF) GPIb binding domain.

DE Von Willebrand Factor; vWF; GPIb binding domain; arteriosclerosis;
KW platelet adhesion inhibitor; stenosis; cerebrovascular injury; human;
KW thrombosis; cardiovascular injury; probe; ss.

XX Homo sapiens.

XX

XX

PN US6008193-A.

XX

PD 28-DEC-1999.

XX

XX

PF 05-JUN-1995; 95US-0463682.

XX

XX

PR 30-NOV-1994; 94US-0347594.

PR

PR 03-SEP-1991; 91US-0753815.

PR

PR 22-JUN-1993; 93US-0080590.

PR

PR 02-MAR-1990; 90US-0487767.

PR

PR 01-MAR-1991; 91WO-US01416.

XX

XX

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX

XX

PI Richter T, Garfinkel L;

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Score: 40.00 Matches: 6
Percent Similarity: 85.71% Conservatives: 0
Best Local Similarity: 85.71% Mismatches: 1
Query Match: 3.62% Indels: 0
DB: 21 Gaps: 0

US-09-375-514-22 (1-205) x AAZ56179 (1-40)

QY 53 ProGlyHisThrProHisPro 59

DB 1 CCAGGACGAGCCACATCCA 21

RESULT 45

AAZ17995

ID AAZ17995 standard; DNA; 40 BP.

XX

XX

AC AAZ17995;

XX

XX

DT 10-DEC-2001 (first entry)

XX

XX

DE A. fumigatus codon optimised phytase gene constructing phy52r PCR primer.

XX

XX

XX

KW Phytase; Pichia cell; heterologous nucleotide; codon optimisation;

KW PCR primer; ss.

XX

XX

OS Aspergillus fumigatus.

OS Synthetic.

XX

XX

PN WO200166693-A1.

XX

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PD 13-SEP-2001.

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Alignment Scores:
Pred. No.: 9.47e+04 Length: 40
Score: 40.00 Matches: 7
Percent Similarity: 66.67% Conservatives: 1
Best Local Similarity: 58.33% Mismatches: 4
Query Match: 3.62% Indels: 0
DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x AAZ17995 (1-40)

Novel Pichia cell useful for producing polypeptide of interest,
comprises a copy of heterologous nucleotide sequence encoding
polypeptide of interest

Example 2; Page 53; 61pp; English.

The invention relates to a Pichia cell comprising at least one copy of
heterologous nucleotide sequence encoding a polypeptide of interest,
where the codon usage of the sequence has been adjusted to match the
preferred codon usage of P. methanolica. The invention also relates to
a method for producing high yields of heterologous codon optimised
polypeptide in a Pichia cell. The Pichia cell is useful for producing
a polypeptide of interest, where the polypeptide is encoded by a
nucleotide sequence heterologous to P. methanolica. The present sequence
is a PCR primer used for constructing Aspergillus fumigatus codon
optimised phytase gene which is the heterologous DNA used in the
invention.

Sequence 40 BP; 9 A; 5 C; 17 G; 9 T; 0 other;

Preventing arteriosclerosis and stenosis using polypeptides derived
from the human von Willebrand factor GPIb binding domain -
Example 1; Column 13; 65pp; English.

This is a probe for the human von Willebrand factor (vWF). The invention
relates to methods of treating arteriosclerosis and stenosis using
polypeptides derived from the human vWF GPIb binding domain. vWF is a
large plasma protein which is synthesised in the endothelial cells of
the blood vessels, and also by megakaryocytes which are the precursors
of platelets. The treatment methods involve the administration of a
polypeptide (see AAY67242 or AAY67243). These polypeptides contain a
fragment of the vWF GPIb binding domain amino acid sequence. The
polypeptides inhibit platelet adhesion and aggregation, therefore the
result of smooth muscle proliferation following vascular injury). The
polypeptides may also be used for treating other cerebrovascular and
cardiovascular injuries and thrombosis.

Sequence 40 BP; 11 A; 14 C; 8 G; 7 T; 0 other;

Alignment Scores:
Pred. No.: 9.47e+04 Length: 40

Qy 186 HsHrTrpIlleGlnAspAsnGlyGlyTrpValGly 197
 ||| :||| |||||
 Db 2 CATGCTAGCTTCAATGGAGGCTGCTGGTGGG 37

RESULT 46

AAL46236/C

ID AAL46236 standard; DNA; 40 BP.

XX

XX

AC AAL46236;

XX

DT 15-AUG-2002 (first entry)

XX

DE Murine growth hormone coding sequence PCR primer SEQ ID NO: 16.

XX

XX Mouse; human; animal model; growth deficiency; cognitive function;

KW growth hormone; IGF-1; osteoporosis; cardiovascular disorder; dwarfism;

KW Illig-type deficiency; Kowarsky syndrome; diabetes; acromegaly;

KW gigantism; glomerulosclerosis; PCR; primer; ss.

XX

OS Mus musculus.

XX

WO200172119-A2.

XX

PD 04-OCT-2001.

XX

PF 02-APR-2001; 2001WO-EP03733.

XX

PR 31-MAR-2000; 2000DE-1016083.

XX

PA (INGE-) INGENIUM PHARM AG.

XX

PI Cornali E, Nehls MC, Schlueter V, Wattler S, Wolf S;

XX

DR WPI; 2001-616425/71.

XX

PT New animal model expressing a modified growth hormone has reduced body

PT weight and size and is useful to determine treatment for growth

PT hormone, particularly IGF-1 related conditions and diseases -

XX

PS Example 6; Page 74; 93pp; English.

XX

CC The present invention relates to a mouse model expressing a modified

CC growth hormone and designated SMAL. The model is used to study diseases,

CC test prospective treatments and identify early detection markers

CC associated with abnormal growth hormone (GH) or IGF-1 activity,

CC particularly dwarfism, Laron syndrome, Illig-type deficiency, Kowarsky

CC syndrome, pituitary gland deficiency, reduced bone mineral density,

CC increased or insufficient body fat accumulation, diabetes, osteoporosis,

CC glomerulosclerosis, gigantism, acromegaly, information processing and

CC cognitive function defects, age-related memory and behaviour deficits,

CC glucose metabolism disorders and cardiovascular disorders. The present

CC sequence is a PCR primer described in the exemplification of the

CC invention.

XX

SQ Sequence 40 BP; 5 A; 15 C; 16 G; 4 T; 0 other;

XX

Alignment Scores:

Pred. No.: 9.47e+04 Length: 40

Score: 40.00 Matches: 7

Percent Similarity: 77.78% Conservative: 0

Best Local Similarity: 77.78% Mismatches: 2

Query Match: 3.62% Indels: 0

DB: 23 Gaps: 0

US-09-375-514-22 (1-205) x AAL46236 (1-40)

Qy 33 GlyAspValGlyAlaAlaProProGly 41

Db ||||| ||||| ||||| |||||

RESULT 47

AAA26253/C

ID AAA26253 standard; DNA; 23 BP.

XX

AC AAA26253;

XX

DT 19-JUL-2000 (first entry)

XX

DE Bcl-2 antisense oligonucleotide sequence SEQ ID NO:2751.

XX

KW Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;

KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;

KW gene expression modification; cancer; phosphorothioate; endonuclease;

KW anticancer; breast cancer; endometrium cancer; ss.

XX

OS Homo sapiens.

XX

PN WO9954459-A2.

XX

PD 28-OCT-1999.

XX

PF 19-APR-1999; 99WO-US08547.

XX

PR 20-APR-1998; 98US-0082404.

XX

PR 23-JUN-1998; 98US-0103636.

XX

PA (RIBO-) RIBOZYME PHARM INC.

XX

PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;

XX

PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;

XX

PI Matulic-Adamic J;

XX

DR WPI; 2000-013248/01.

XX

XX New nucleic acids that interact, and optionally cleave, target

XX sequences, used to treat cancer -

XX

PS Example 9; Page 106; 148pp; English.

XX

XX The present invention describes nucleic acids (A) that interact stably

XX with a target sequence and contain at least one phosphoro(dithioate

XX link, having endonuclease activity. (A), and more generally any

XX catalytic nucleic acid (A') that modulates expression of the oestrogen

XX receptor gene, are used to treat cancer (particularly of breast or

XX endometrium), in vivo or by transforming cells ex vivo and implanting

XX treated cells, or for other conditions associated with levels of

XX oestrogen receptor. Because of the high selectivity for targeted RNA, (A)

XX can also be used to correlate inhibition of gene expression with

XX alterations in phenotype, particularly for identification of therapeutic

XX targets, and as research reagents (for RNA, in the same way that

XX restriction endonucleases are used with DNA). The combination of

XX modifications in (A) improves resistance to nucleases, binding affinity

XX and/or activity. AAA23503 to AAA24747 represent oestrogen receptor

XX hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their

XX corresponding target sequences. AAA25993 to AAA26105 represent oestrogen

XX receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent

XX their corresponding target sequences. AAA26219 to AAA26271 represent

XX other ribozyme sequences and antisense oligonucleotides used in the

XX exemplification of the present invention.

XX

SQ Sequence 23 BP; 9 A; 9 C; 4 G; 1 T; 0 other;

XX

Alignment Scores:

Pred. No.: 6.27e+04 Length: 23

Score: 39.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.53% Indels: 0

DB: 21 Gaps: 0

US-09-375-514-22 (1-205) x AAA26253 (1-23)

Qy 149 AlaPhePheGluPheGlyGly 155

Db ||||| ||||| ||||| |||||

21 GCCTTCTTTCGAGTTCGGTGGG 1

cc: [REDACTED]

Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.

us-09-375-514-22.rng

Sun Jun 1 14:56:00 2003

OS Homo sapiens.
 OS Synthetic.
 XX WO200142459-A1.
 PN
 XX
 XX 14-JUN-2001.
 PD
 XX 07-DEC-2000; 2000WO-JP08667.
 PF
 XX 09-DEC-1999; 99JP-0350427.
 PR
 XX (HISM) HISAMITSU PHARM CO LTD.
 PA
 XX Shibazaki F, Kuma H;
 PI
 XX WPI; 2001-381681/40.
 DR
 XX New apoptosis inhibitors, useful for treating apoptosis related
 PT disorders -
 PT
 XX Example 1; Page 11; 43pp; Japanese.
 PS
 XX The invention relates to an apoptosis inhibitor comprising the
 CC amino acid sequence of Bcl-2 protein in which at least one serine
 CC residue is substituted by alanine or aspartic acid. The protein has
 CC increased apoptosis inhibitory activity compared with the wild type
 CC Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment
 CC of disorders caused by apoptosis. The present sequence was used to
 CC create a mutant Bcl-2 protein of the invention.
 CC
 XX Sequence 27 BP; 5 A; 8 C; 9 G; 5 T; 0 other;
 SQ

Alignment Scores:
 Pred. No.: 7.38e+04 Length: 27
 Score: 39.00 Matches: 8
 Percent Similarity: 88.89% Conservative: 0
 Best Local Similarity: 88.89% Mismatches: 1
 Query Match: 3.53% Indels: 0
 DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x AAH45303 (1-27)
 Qy 112 PheAlaGluMetSerSerGlnLeuHis 120
 Db 27 TTCGCCGAGATGGTCAGCCAGCTGCAC 1

Search completed: May 31, 2003, 22:29:38
 Job time : 222 secs

212	19.4	0.4	27	6	A63581	A63581 Sequence 22	285	19	0.4	40	6	AX235336	AX235336 Sequence
213	19.4	0.4	30	6	A43129	A43129 Sequence 15	c 286	19	0.4	40	6	AX299737	AX299737 Sequence
214	19.4	0.4	30	6	AX351711	AX351711 Sequence	287	18.8	0.4	22	6	AX031293	AX031293 Sequence
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ORGANISM
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Method for detecting mutations in nucleotide sequences
JOURNAL Patent: WO 0212553-A 28 14-FEB-2002;
Nanogen Recognomics GmbH (DE)
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DEFINITION Sequence 29 from Patent WO0212553.
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DEFINITION Sequence 2 from patent US 5750390.
ACCESSION AR007288

AR007288.1 GI:3966772
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 37)
AUTHORS Thompson,J.D. and Draper,K.G.
TITLE Method and reagent for treatment of diseases caused by expression of the bcl-2 gene
JOURNAL Patent: US 5750390-A 2 12-MAY-1998;
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ACCESSION AX377550
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SOURCE Homo sapiens
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Method for detecting mutations in nucleotide sequences
JOURNAL Patent: WO 0212553-A 27 14-FEB-2002;
Nanogen Recognomics GmbH (DE)
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Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1615 CCCGGGCACACGCCGCCATCCAGCGCATCCCGGACC 1651
|||||
Db 39 CCCGGGCACACGCCGCCATCCAGCGCATCCCGGACC 3
RESULT 5
AR007301
LOCUS AR007301 36 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 15 from patent US 5750390.
ACCESSION AR007301
VERSION AR007301.1 GI:3966785
KEYWORDS Unknown.
SOURCE Unclassified.
REFERENCE 1 (bases 1 to 36)
AUTHORS Thompson,J.D. and Draper,K.G.
TITLE Method and reagent for treatment of diseases caused by expression of the bcl-2 gene
JOURNAL Patent: US 5750390-A 15 12-MAY-1998;

FEATURES source Location/Qualifiers
BASE COUNT 10 a 13 c 8 g 5 t
ORIGIN

Query Match 0.7%; Score 36; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1997 ACCTGAACCGCACCTGCACACCTGGATCCAGGATA 2032
|||||
Db 1 ACCTGAACCGCACCTGCACACCTGGATCCAGGATA 36
|||||

RESULT 6
AR007306
LOCUS
DEFINITION Sequence 20 from patent US 5750390.
ACCESSION AR007306
VERSION AR007306.1 GI:3966790
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Thompson, J.D. and Draper, K.G.
TITLE Method and reagent for treatment of diseases caused by expression of the bcl-2 gene
JOURNAL Patent: US 5750390-A 20 12-MAY-1998;
FEATURES Location/Qualifiers
source 1. .35
BASE COUNT 14 a 10 c 6 g 5 t
ORIGIN

Query Match 0.7%; Score 35; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2180 GTCACATGCTGCTGCCCAACAATATGCAAGG 2214
|||||
Db 1 GTCACATGCTGCTGCCCAACAATATGCAAGG 35
|||||

RESULT 7
AR052604
LOCUS
DEFINITION Sequence 2 from patent US 5831066.
ACCESSION AR052604
VERSION AR052604.1 GI:5975968
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 2 03-NOV-1998;
FEATURES Location/Qualifiers
source 1. .35
BASE COUNT 6 a 8 c 13 g 8 t
ORIGIN

Query Match 0.7%; Score 35; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1442 CTTTCTCTCTGGGAAGGATGCGCACCGTGGGAGA 1476
|||||
Db 1 CTTTCTCTCTGGGAAGGATGCGCACCGTGGGAGA 35
|||||

RESULT 8
I96083
LOCUS
DEFINITION Sequence 2 from patent US 5734033.
ACCESSION I96083
VERSION I96083.1 GI:3940553
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Reed, J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 2 31-MAR-1998;
FEATURES Location/Qualifiers
source 1. .35
BASE COUNT 6 a 8 c 13 g 8 t
ORIGIN

Query Match 0.7%; Score 35; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1442 CTTTCTCTCTGGGAAGGATGCGCACCGTGGGAGA 1476
|||||
Db 1 CTTTCTCTCTGGGAAGGATGCGCACCGTGGGAGA 35
|||||

RESULT 9
AR007302
LOCUS
DEFINITION Sequence 16 from patent US 5750390.
ACCESSION AR007302
VERSION AR007302.1 GI:3966786
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 34)
AUTHORS Thompson, J.D. and Draper, K.G.
TITLE Method and reagent for treatment of diseases caused by expression of the bcl-2 gene
JOURNAL Patent: US 5750390-A 16 12-MAY-1998;
FEATURES Location/Qualifiers
source 1. /34
BASE COUNT 6 a 9 c 11 g 8 t
ORIGIN

Query Match 0.7%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2043 GGATGCTTTGTGGAACTGTACGGCCCCCAGCATG 2076
|||||
Db 1 GGATGCTTTGTGGAACTGTACGGCCCCCAGCATG 34
|||||

RESULT 10
AR007307
LOCUS
DEFINITION Sequence 21 from patent US 5750390.
ACCESSION AR007307
VERSION AR007307.1 GI:3966791
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 34)
AUTHORS Thompson, J.D. and Draper, K.G.
TITLE Method and reagent for treatment of diseases caused by expression

of the bcl-2 gene
Patent: US 5750390-A 21 12-MAY-1998;
Location/Qualifiers

FEATURES
source
1. .34

BASE COUNT
ORIGIN
14 a 5 c 6 g 9 t

Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e+04; Length 34;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2235 AATATGCAATTCAGTGTACCATGAACAAA 2268

Db 1 AATATGCAATTCAGTGTACCATGAACAAA 34

RESULT 11
LOCUS A56864 33 bp DNA PAT 03-MAR-1998
DEFINITION Sequence 43 from Patent WO9627663.
ACCESSION A56864
VERSION A56864.1 GI:3712876

KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 33)
AUTHORS Capaccioli, S., Morelli, S. and Nicolin, A.

TITLE AN ANTISENSE TRANSCRIPT ASSOCIATED TO TUMOR CELLS HAVING A T(14;18) TRANSLOCATION AND OLIGODEOXYNUCLEOTIDES USEFUL IN THE DIAGNOSIS AND TREATMENT OF SAID TUMOR CELLS

JOURNAL Patent: WO 9627663-A 43 12-SEP-1996;
COMMENT CONSIGLIO NAZIONALE RICERCA (IT)

FEATURES
source
1. .33
Location/Qualifiers

BASE COUNT
ORIGIN
9 a 6 c 6 g 12 t

Query Match
Best Local Similarity 100.0%; Pred. No. 4e+04; Length 33;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4289 GCAATTCGGCATTTAATTCATGATTCAGGAT 4321

Db 1 GCAATTCGGCATTTAATTCATGATTCAGGAT 33

RESULT 12
LOCUS AR007291 33 bp DNA PAT 04-DEC-1998

DEFINITION Sequence 5 from patent US 5750390.
ACCESSION AR007291

VERSION AR007291.1 GI:39666775

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 33)
AUTHORS Thompson, J.D. and Draper, K.G.

TITLE Method and reagent for treatment of diseases caused by expression of the bcl-2 gene

JOURNAL Patent: US 5750390-A 5 12-MAY-1998;
FEATURES Location/Qualifiers

source
1. .33
/organism="unknown"

BASE COUNT
ORIGIN
5 a 16 c 7 g 5 t

Query Match
Score 0.6%; Length 33; DB 6; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 4e+04; Length 33;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1592 CACCGGGCATCTTCTCTCCAGCCGGGCACA 1624

Db 1 CACCGGGCATCTTCTCTCCAGCCGGGCACA 33

RESULT 13
LOCUS AR096260 33 bp DNA PAT 08-SEP-2000

DEFINITION Sequence 44 from patent US 6005095.
ACCESSION AR096260

VERSION AR096260.1 GI:10024906

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 33)
AUTHORS Capaccioli, S., Morelli, S. and Nicolin, A.

TITLE Antisense transcript associated to tumor cells having a T(14;18) translocation and oligodeoxynucleotides useful in the diagnosis and treatment of said tumor cells

JOURNAL Patent: US 6005095-A 44 21-DEC-1999;
FEATURES Location/Qualifiers

source
1. .33
/organism="unknown"

BASE COUNT
ORIGIN
9 a 6 c 6 g 12 t

Query Match
Best Local Similarity 100.0%; Pred. No. 4e+04; Length 33;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4289 GCAATTCGGCATTTAATTCATGATTCAGGAT 4321

Db 1 GCAATTCGGCATTTAATTCATGATTCAGGAT 33

RESULT 14
LOCUS AX207593 36 bp DNA PAT 31-AUG-2001

DEFINITION Sequence 2 from Patent WO0157205.
ACCESSION AX207593

VERSION AX207593.1 GI:15422299

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 36)
AUTHORS Shir, A. and Levitzky, A.

TITLE Selective killing of cells by activation of double-stranded rna dependent protein kinase-pkr

JOURNAL Patent: WO 0157205-A 2 09-AUG-2001;
Yissum Research and Development Co., Hebrew University of Jerusalem (IL)

FEATURES
source
Location/Qualifiers

1. .136
/organism="Homo sapiens"
/db|xref="taxon:9606"

BASE COUNT
ORIGIN
15 a 4 c 10 g 7 t

Query Match
Best Local Similarity 94.4%; Pred. No. 4.5e+04; Length 36;
Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4098 CAAAGCATCTCTGAGAGGTGAGATAGCCCTGAGT 4133

Db 1 CAAAGCATCTCTGAGAGGTGAGATAGCCCTGAGT 36

Query Match 0.6%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.7e+05;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1729 CCTGTGTCACCTGGCCCTCGCCAAAS 1756

Db 1 CCTGTGTCACCTGGCCCTCGCCAAAG 28

RESULT 20

A56841/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 4504

Db 30

CTTCAGGGTCTTCTGAAATGCAGTGGT 4531

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Query Match 0.6%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.7e+05;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1729 CCTGTGTCACCTGGCCCTCGCCAAAS 1756

Db 1 CCTGTGTCACCTGGCCCTCGCCAAAG 28

RESULT 20

A56841/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 4504

Db 30

CTTCAGGGTCTTCTGAAATGCAGTGGT 4531

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Query Match 0.6%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.7e+05;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1729 CCTGTGTCACCTGGCCCTCGCCAAAS 1756

Db 1 CCTGTGTCACCTGGCCCTCGCCAAAG 28

RESULT 20

A56841/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 4504

Db 30

CTTCAGGGTCTTCTGAAATGCAGTGGT 4531

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KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 40)
AUTHORS       Weber,J.L.,
TITLE         Length polymorphisms in (dc-da).sub.n.(dg-dt).sub.n sequences and method of using the same
JOURNAL       Patent: US 5582979-A 403 10-DEC-1996;
FEATURES      Location/Qualifiers
               source
                 1..40
                   /organism="unknown"
BASE COUNT    20 a   20 c   0 g   0 t
ORIGIN

Query Match          0.5%; Score 27.2; DB 6; Length 40;
Best Local Similarity 80.0%; Pred.No. 5.5e+05;
Matches 32; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2310 CACACACAGCACGACACACACACACACACAATTAACA 2349
||||| |||| | ||||| ||||| ||||| ||||| ||||| 
Db 1 CACACACACACACACACACACACACACACACACACACA 40


RESULT 27
A22453 A22453 27 bp DNA linear PAT 24-NOV-1994
LOCUS MBR reporter probe.
DEFINITION A22453
ACCESSION A22453
VERSION A22453.1 GI:641507
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequenes.
FEATURES location/Qualifiers
source 1..27
/db_xref="taxon:32630"
/organism="synthetic construct"
BASE COUNT 8 a 12 c 3 g 4 t
ORIGIN

Query Match          0.5%; Score 27; DB 6; Length 27;
Best Local Similarity 100.0%; Pred.No. 5.7e+05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4440 TTTCACACAGACCACCCAGGCCCT 4466
||||| ||||| ||||| ||||| ||||| ||||| ||||| 
Db 1 TTTCACACAGACCACCCAGGCCCT 27


RESULT 28
AR007303 AR007303 27 bp DNA linear PAT 04-DEC-1998
LOCUS Sequence 17 from patent US 5750390.
DEFINITION ACCESSION AR007303
ACCESSION AR007303
VERSION AR007303.1 GI:39666787
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Thompson,J.D. and Draper,K.G.
TITLE Method and reagent for treatment of diseases caused by expression of the bcl-2 gene
JOURNAL Patent: US 5750390-A 17 12-MAY-1998;
FEATURES Location/Qualifiers
source 1..27
/organism="unknown"
BASE COUNT 1 a 8 c 5 g 13 t
ORIGIN

Query Match          0.5%; Score 27; DB 6; Length 27;
Best Local Similarity 100.0%; Pred.No. 5.7e+05;
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	Matches	27;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	2081	CCCTGTTTGA	TTCTCCTGGCTGTC	2107						
Db	1	CCCTGTTTGA	TTCTCCTGGCTGTC	27						

RESULT 29			
I31303			
LOCUS	I31303	31 bp	DNA
DEFINITION	Sequence 215 from patent US 5582979.		
ACCESSION	I31303		linear
VERSION	I31303.1	GI:18222094	PAT 06-FEB-1997

Unknown:
Unclassified.
1 (bases 1 to 31)
Weber, J. L.
Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
method of using the same
Patent: US 5582979-A 215 10-DEC-1996;
Location/Qualifiers
1. .31
source

Query Match 0.5%; Score 26.8; DB 6; Length 31;
Best Local Similarity 93.3%; Pred. No. 6.4e+05;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 31)
Weber, J.L.
Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
method of using the same
Patent: US 5582979-A 271 10-DEC-1996;
Location/Qualifiers
1..31
/organism="unknown"
16 a 15 c 0 g
BASE COUNT
0 t

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Query Match      0.5%; Score 26.8; DB 6; Length 31;
Best Local Similarity 93.3%; Pred. No. 6.4e+05;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACAGAGACACACACACACACA 2339
      ||||| ||||| ||||| ||||| |||||
Db 2 CACACACACACACACACACACACACACA 31

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RESULT 32	E32203	32 bp	DNA	
LOCUS	E32203		linear	PAT 18-JUN-2001
DEFINITION	Method for isolating satellite sequence.			
ACCESSION	E32203			
VERSION	E32203.1	GI:13021740		
KEYWORDS	JP 2000060559-A/5.			
SOURCE	Haliotis discus discus			
ORGANISM	Haliotis discus discus			
	Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;			
	Haliotidae; Haliotis.			

RESULT 30		PAT 06-FEB-1997	AUTHORS Hideaki,T. and Masashi,S.
I31323 LOCUS	linear		TITLE Method for isolating satellite sequence
I31323			JOURNAL
Sequence 235 from patent US 582979.			Patent: JP 2000060559-A 5 29-FEB-2000;
I31323 ACCESSION			Natl INST OF AGRIC BIOLOGICAL RESOURCES
I31323.1 GI:1822114			OS Hallotis discus discus
. KEYWORDS			PN JP 2000060559-A/5
SOURCE			PD 29-FEB-2000
Unknown.			PF 18-AUG-1998 JP 1998232153
ORGANISM			PR
Unkown.			PI HIDEAKI TAKAHASHI,MASASHI SEKINO
Unclassified,			PC C12N15/09,C12Q1/68,C12N15/00
1 /bases 1 to 31)			
REFERENCE			

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// TITLE
Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
method of using the same
Patent: US 5582979-A 235 10-DEC-1996;
FEATURES
    source
        1..31
        /organism="unknown"
    16 a 15 c 0 g 0 t
BASE COUNT
ORIGIN
    /organism="Haliotis discus discus"
    /db_xref="taxon:91233"
    16 a 16 c 0 g 0 t
FT
    source
        1..32
        /organism="Haliotis discus discus"
    16 a 16 c 0 g 0 t
    key
        1..32
        /organism="Haliotis discus discus"
    16 a 16 c 0 g 0 t

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[illegible][illegible]

[illegible]

83	26.8	0.5	38	24	ABK24299	Human microsatelli	c 156	23.8	0.5	27	13	AAQ34181	Microsatellite seq
c 84	26.8	0.5	39	13	AAQ33648	Microsatellite seq	c 157	23.8	0.5	27	13	AAQ33678	Microsatellite seq
c 85	26.8	0.5	39	13	AAQ33807	Microsatellite seq	c 158	23.8	0.5	27	13	AAQ33804	Microsatellite seq
c 86	26.8	0.5	39	13	AAQ33825	Microsatellite seq	c 159	23.8	0.5	27	16	AAQ83951	Oligonucleotide cl
c 87	26.8	0.5	39	13	AAQ33971	Microsatellite seq	c 160	23.8	0.5	27	18	AAQ65733	Repeat sequence fr
c 88	26.8	0.5	39	18	AAQ5731	Repeat sequence fr	c 161	23.8	0.5	27	22	AAH24300	Synthetic antineop
c 89	26.8	0.5	39	18	AAQ5714	Repeat sequence fr	c 162	23.8	0.5	27	22	AAH45303	Human Bcl-2 mutage
c 90	26.8	0.5	40	13	AAQ34091	Sequence of a micr	c 163	23.8	0.5	27	22	AAH45305	Human Bcl-2 mutage
c 91	26.8	0.5	40	18	AAQ5725	Repeat sequence fr	c 164	23.8	0.5	27	22	AAH45306	Human Bcl-2 mutage
c 92	26.8	0.5	40	18	AAQ66051	(dC-dA)n.(dG-dT)n	c 165	23.8	0.5	27	22	AAH46001	Synthetic oligonuc
c 93	26.4	0.5	38	13	AAQ33843	Microsatellite seq	c 166	23.8	0.5	27	22	AAH46005	Synthetic oligonuc
c 94	26.4	0.5	36	13	AAQ34107	Sequence of a micr	c 167	23.8	0.5	27	22	AAH6017	Oligonucleotide cl
c 95	26.2	0.5	29	21	AAQ65050	Human bcl genes an	c 168	23.8	0.5	27	22	AAH60473	Oligonucleotide cl
c 96	26.2	0.5	40	18	AAQ5736	Repeat sequence fr	c 169	23.8	0.5	36	16	AAQ83935	Oligonucleotide cl
c 97	26	0.5	34	13	AAQ33734	Microsatellite seq	c 170	23.6	0.5	33	13	AAQ33944	Microsatellite seq
c 98	25.8	0.5	29	13	AAQ33687	Microsatellite seq	c 171	23.6	0.5	37	13	AAQ33698	Microsatellite seq
c 99	25.8	0.5	29	13	AAQ33846	Microsatellite seq	c 172	23.6	0.5	38	13	AAQ33767	Microsatellite seq
c 100	25.8	0.5	29	13	AAQ33956	Microsatellite seq	c 173	23.2	0.5	28	13	AAQ34074	Microsatellite seq
c 101	25.8	0.5	29	16	AAQ33977	Microsatellite seq	c 174	23.2	0.5	28	13	AAQ33933	Microsatellite seq
c 102	25.8	0.5	29	13	AAQ83953	Oligonucleotide cl	c 175	23.2	0.5	29	13	AAQ33630	Microsatellite seq
c 103	25.8	0.5	29	18	AAQ5712	Repeat sequence fr	c 176	23.2	0.5	32	13	AAQ34149	Sequence of a micr
c 104	25.8	0.5	29	18	AAQ5712	Repeat sequence fr	c 177	23.2	0.5	37	13	AAQ34184	Microsatellite seq
c 105	25.8	0.5	29	22	AAQ60474	Oligonucleotide cl	c 178	23	0.5	23	14	AAQ51950	Bcl-2 mRNA ribozym
c 106	25.8	0.5	30	18	AAQ5789	Repeat sequence fr	c 179	23	0.5	23	21	AAQ26253	Bcl-2 antisense ol
c 107	25.8	0.5	30	23	AAQ33787	Simple sequence re	c 180	23	0.5	23	21	AAQ26255	Bcl-2 antisense ol
c 108	25.8	0.5	30	24	AAQ42354	Novel sand pear ml	c 181	23	0.5	36	17	AAQ35026	Triplex-forming ol
c 109	25.8	0.5	39	18	AAQ5775	Repeat sequence fr	c 182	22.8	0.4	26	13	AAQ34083	Microsatellite seq
c 110	25.4	0.5	27	22	AAH45300	Human Bcl-2 mutage	c 183	22.8	0.4	26	13	AAQ33684	Microsatellite seq
c 111	25.4	0.5	27	22	AAH45302	Human Bcl-2 mutage	c 184	22.8	0.4	26	13	AAQ33704	Microsatellite seq
c 112	25.4	0.5	35	13	AAQ33695	Microsatellite seq	c 185	22.8	0.4	26	13	AAQ33831	Microsatellite seq
c 113	25.2	0.5	32	13	AAQ34119	Microsatellite seq	c 186	22.8	0.4	26	13	AAQ33837	Microsatellite seq
c 114	25.2	0.5	32	18	AAQ66057	Sequence of a micr	c 187	22.8	0.4	26	22	AAI64469	SSR motif #19. Un
c 115	25.2	0.5	37	13	AAQ33669	(dC-dA)n.(dG-dT)n	c 188	22.6	0.4	40	21	AAQ26060	Polynucleotide seq
c 116	25	0.5	25	13	AAQ22742	Microsatellite seq	c 189	22.4	0.4	24	17	AAQ36054	bcl-2 reverse PCR
c 117	25	0.5	25	21	AAQ73296	Primer bcl-2 adjac	c 190	22.4	0.4	24	20	AAQ26250	Reverse primer for
c 118	25	0.5	25	21	AAQ73297	Bcl-2 specific gen	c 191	22.4	0.4	24	20	AAQ81830	Mouse bcl-2 revers
c 119	24.8	0.5	28	13	AAQ34027	Microsatellite seq	c 192	22.4	0.4	24	21	AAQ88587	PCR primer for mou
c 120	24.8	0.5	28	13	AAQ34035	Microsatellite seq	c 193	22.4	0.4	24	21	AAQ89800	Reverse primer for
c 121	24.8	0.5	28	13	AAQ34161	Sequence of a micr	c 194	22.4	0.4	24	21	AAQ88011	Mouse bcl-2 revers
c 122	24.8	0.5	28	13	AAQ33645	Microsatellite seq	c 195	22.4	0.4	24	22	AAQ26285	Human BCL-2 PCR pr
c 123	24.8	0.5	28	18	AAQ66102	Repeat sequence fo	c 196	22.4	0.4	26	21	AAQ26251	Bcl-2 antisense ol
c 124	24.8	0.5	28	23	AAQ33711	Simple sequence re	c 197	22.4	0.4	40	24	ABK94443	Human BRCAL/hMLH1
c 125	24.6	0.5	40	13	AAQ25030	Oligonucleotide sp	c 198	22.2	0.4	27	13	AAQ34077	Microsatellite seq
c 126	24.4	0.5	34	14	AAQ36324	NGFR target sequen	c 199	22.2	0.4	27	13	AAQ45077	Human Bcl-2 mutage
c 127	24.2	0.5	30	21	AAQ39502	H. discus derived	c 200	22.2	0.4	27	22	AAH45298	Human Bcl-2 mutage
c 128	24.2	0.5	33	13	AAQ33731	Microsatellite seq	c 201	22.2	0.4	27	22	AAH45301	Human Bcl-2 mutage
c 129	24.2	0.5	37	13	AAQ33710	Microsatellite seq	c 202	22.2	0.4	27	22	AAH45304	Human Bcl-2 mutage
c 130	24	0.5	24	13	AAQ30093	MBR primer for Maj	c 203	22	0.4	22	14	AAQ49816	Bcl-2 antisense ol
c 131	24	0.5	24	16	AAQ86624	Bcl-2 chromosomal	c 204	22	0.4	22	14	AAQ49817	Bcl-2 antisense ol
c 132	24	0.5	24	16	AAQ86625	Bcl-2 chromosomal	c 205	22	0.4	22	14	AAQ51952	BCL-2 mRNA ribozym
c 133	24	0.5	24	17	AAQ42415	BCL-2 chromosomal	c 206	22	0.4	22	16	AAQ01266	bcl-2 gene specifi
c 134	24	0.5	24	17	AAQ42416	BCL-2 chromosomal	c 207	22	0.4	22	16	AAQ01267	bcl-2 gene specifi
c 135	24	0.5	24	17	AAQ15569	BCL-2 chromosomal	c 208	22	0.4	22	17	AAQ17218	Target primer 3 fo
c 136	24	0.5	24	17	AAQ15570	BCL-2 chromosomal	c 209	22	0.4	22	21	AAQ65038	Bcl2 RNA Rn-PCR pr
c 137	24	0.5	24	19	AAQ66348	BCL-2 chromosomal	c 210	22	0.4	28	18	AAQ79848	Human bcl-2 gene n
c 138	24	0.5	24	19	AAQ66347	BCL-2 chromosomal	c 211	22	0.4	30	19	AAQ05323	PCR primer 2 used
c 139	24	0.5	24	20	AAQ23189	BCL-2 chromosomal	c 212	22	0.4	33	18	AAQ65770	Repeat sequence fr
c 140	24	0.5	24	20	AAQ23190	BCL-2 t(14:18) pro	c 213	21.8	0.4	35	13	AAQ34021	Microsatellite seq
c 141	24	0.5	24	21	AAQ76092	BCL-2 t(14:18) pro	c 214	21.8	0.4	25	13	AAQ33642	Microsatellite seq
c 142	24	0.5	24	22	AAQ12909	PCR primer PAL for	c 215	21.8	0.4	25	13	AAQ33861	Microsatellite seq
c 143	24	0.5	24	22	AAQ82684	Human BCL-2 PCR pr	c 216	21.8	0.4	25	13	AAQ33918	Microsatellite seq
c 144	24	0.5	24	24	ABN85362	Bcl-2 related olig	c 217	21.8	0.4	25	18	AAQ65734	Repeat sequence fr
c 145	24	0.5	24	24	ABK52487	Fluorescent probe	c 218	21.8	0.4	25	22	AAH38303	SNP specific SNPE
c 146	24	0.5	24	24	ABK88835	Human bcl-2 PCR pr	c 219	21.8	0.4	26	14	AAQ47179	MHC DR A intron bi
c 147	24	0.5	24	24	ABK15646	Bcl-2 RNA-DNA hybr	c 220	21.8	0.4	28	18	AAQ79847	Human bcl-2 gene n
c 148	24	0.5	24	24	ABK15648	Bcl-2 RNA-DNA hybr	c 221	21.8	0.4	33	18	AAQ96579	Mouse bcl-w gene p
c 149	24	0.5	32	22	AAH45308	Human Bcl-2 PCR pr	c 222	21.6	0.4	31	21	AAQ50360	Bcl2 gene 3' PCR p
c 150	24	0.5	36	16	AAQ86648	Bcl-2 splice accep	c 223	21.6	0.4	34	13	AAQ33924	Microsatellite seq
c 151	24	0.5	36	19	AAQ19656	Human bcl-2 oligon	c 224	21.4	0.4	33	15	AAQ73441	Crohn's disease/ul
c 152	24	0.5	36	24	ABL54154	Bcl-2 antisense ol	c 225	21.2	0.4	27	13	AAQ33740	Microsatellite seq
c 153	23.8	0.5	27	13	AAQ34012	Microsatellite seq	c 226	21.2	0.4	28	14	AAQ46987	First type iii-C a
c 154	23.8	0.5	27	13	AAQ34044	Microsatellite seq	c 227	21.2	0.4	28	18	AAQ71141	Fibronectin fragme
c 155	23.8	0.5	27	13	AAQ34143	Sequence of a micr	c 228	21.2	0.4	28	19	AAQ28773	Fibronectin PCR 3'

c 229	21.2	0.4	28	20	AAV69809	Human fibronectin	302	20	0.4	20	22	AA15638	Human Bcl-2 protei
c 230	21.2	0.4	33	22	AAH77493	Human zinc finger	303	20	0.4	20	22	AA15639	Human Bcl-2 protei
c 231	21	0.4	21	24	ABN85360	Bcl-2 related olig	304	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 232	21	0.4	21	24	ABN85361	Bcl-2 related olig	305	20	0.4	20	22	AA15641	Human Bcl-2 protei
c 233	21	0.4	31	18	AA196580	Mouse bcl-w gene p	306	20	0.4	20	22	AA15642	Human Bcl-2 protei
c 234	21	0.4	33	14	AAQ41697	Rat serotonin regi	307	20	0.4	20	22	AA15643	Human Bcl-2 protei
c 235	21	0.4	35	16	AAQ87895	Normalised library	308	20	0.4	20	22	AA15646	Human Bcl-2 protei
c 236	21	0.4	35	16	AAQ87896	Normalised library	309	20	0.4	20	22	AA15647	Human Bcl-2 protei
c 237	21	0.4	38	22	AA107487	Human reproductive	c 310	20	0.4	20	22	AA15648	Human Bcl-2 protei
c 238	21	0.4	40	13	AAQ34094	Sequence of a micr	311	20	0.4	20	22	AA15649	Human Bcl-2 protei
c 239	20.8	0.4	24	13	AAQ34094	Microsatellite seq	c 312	20	0.4	20	22	AA15650	Human Bcl-2 protei
c 240	20.8	0.4	24	13	AAQ34094	Microsatellite seq	313	20	0.4	20	22	AA15651	Human Bcl-2 protei
c 241	20.8	0.4	24	13	AAQ34094	Microsatellite seq	c 315	20	0.4	20	22	AA15652	Human Bcl-2 protei
c 242	20.8	0.4	24	13	AAQ34094	Microsatellite seq	c 316	20	0.4	20	22	AA15653	Human Bcl-2 protei
c 243	20.8	0.4	24	13	AAQ34094	Microsatellite seq	c 317	20	0.4	20	22	AA15654	Human Bcl-2 protei
c 244	20.8	0.4	24	13	AAQ34094	Microsatellite seq	c 318	20	0.4	20	22	AA15655	Human Bcl-2 protei
c 245	20.8	0.4	24	16	AA162762	Repeat sequence fo	c 319	20	0.4	20	22	AA15656	Human Bcl-2 protei
c 246	20.8	0.4	24	18	AA162762	Repeat sequence fo	c 320	20	0.4	20	22	AA15657	Human Bcl-2 protei
c 247	20.8	0.4	24	22	AA162762	Repeat sequence fo	c 321	20	0.4	20	22	AA15658	Human Bcl-2 protei
c 248	20.8	0.4	24	22	AA162762	Repeat sequence fo	c 322	20	0.4	20	22	AA15659	Human Bcl-2 protei
c 249	20.8	0.4	24	22	AA162762	Repeat sequence fo	c 323	20	0.4	20	22	AA15660	Human Bcl-2 protei
c 250	20.8	0.4	24	22	AA162762	Repeat sequence fo	c 324	20	0.4	20	22	AA15661	Human Bcl-2 protei
c 251	20.8	0.4	24	22	AA162762	Repeat sequence fo	c 325	20	0.4	20	22	AA15662	Human Bcl-2 protei
c 252	20.8	0.4	24	22	AA162762	Repeat sequence fo	c 326	20	0.4	20	22	AA15663	Human Bcl-2 protei
c 253	20.8	0.4	24	22	AA162762	Repeat sequence fo	c 327	20	0.4	20	22	AA15664	Human Bcl-2 protei
c 254	20.6	0.4	27	17	AA162762	Repeat sequence fo	c 328	20	0.4	20	22	AA15665	Human Bcl-2 protei
c 255	20.6	0.4	27	17	AA162762	Repeat sequence fo	c 329	20	0.4	20	22	AA15666	Human Bcl-2 protei
c 256	20.6	0.4	27	17	AA162762	Repeat sequence fo	c 330	20	0.4	20	22	AA15667	Human Bcl-2 protei
c 257	20.6	0.4	27	17	AA162762	Repeat sequence fo	c 331	20	0.4	20	22	AA15668	Human Bcl-2 protei
c 258	20.6	0.4	27	17	AA162762	Repeat sequence fo	c 332	20	0.4	20	22	AA15669	Human Bcl-2 protei
c 259	20.4	0.4	27	17	AA162762	Repeat sequence fo	c 333	20	0.4	20	22	AA15670	Human Bcl-2 protei
c 260	20.4	0.4	27	17	AA162762	Repeat sequence fo	c 334	20	0.4	20	22	AA15671	Human Bcl-2 protei
c 261	20.4	0.4	27	17	AA162762	Repeat sequence fo	c 335	20	0.4	20	22	AA15672	Human Bcl-2 protei
c 262	20.4	0.4	27	17	AA162762	Repeat sequence fo	c 336	20	0.4	20	22	AA15673	Human Bcl-2 protei
c 263	20.4	0.4	27	17	AA162762	Repeat sequence fo	c 337	20	0.4	20	22	AA15674	Human Bcl-2 protei
c 264	20.4	0.4	27	17	AA162762	Repeat sequence fo	c 338	20	0.4	20	22	AA15675	Human Bcl-2 protei
c 265	20.2	0.4	26	14	AAQ44016	Human p70 ribosome	c 339	20	0.4	20	22	AA15676	Human Bcl-2 protei
c 266	20.2	0.4	26	14	AAQ44016	Human p70 ribosome	c 340	20	0.4	20	22	AA15677	Human Bcl-2 protei
c 267	20.2	0.4	26	14	AAQ44016	Human p70 ribosome	c 341	20	0.4	20	22	AA15678	Human Bcl-2 protei
c 268	20.2	0.4	26	14	AAQ44016	Human p70 ribosome	c 342	20	0.4	20	22	AA15679	Human Bcl-2 protei
c 269	20.2	0.4	26	14	AAQ44016	Human p70 ribosome	c 343	20	0.4	20	22	AA15680	Human Bcl-2 protei
c 270	20.2	0.4	26	14	AAQ44016	Human p70 ribosome	c 344	20	0.4	20	22	AA15681	Human Bcl-2 protei
c 271	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 345	20	0.4	20	22	AA15682	Human Bcl-2 protei
c 272	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 346	20	0.4	20	22	AA15683	Human Bcl-2 protei
c 273	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 347	20	0.4	20	22	AA15684	Human Bcl-2 protei
c 274	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 348	20	0.4	20	22	AA15685	Human Bcl-2 protei
c 275	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 349	20	0.4	20	22	AA15686	Human Bcl-2 protei
c 276	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 350	20	0.4	20	22	AA15687	Human Bcl-2 protei
c 277	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 351	20	0.4	20	22	AA15688	Human Bcl-2 protei
c 278	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 352	20	0.4	20	22	AA15689	Human Bcl-2 protei
c 279	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 353	20	0.4	20	22	AA15690	Human Bcl-2 protei
c 280	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 354	20	0.4	20	22	AA15691	Human Bcl-2 protei
c 281	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 355	20	0.4	20	22	AA15692	Human Bcl-2 protei
c 282	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 356	20	0.4	20	22	AA15693	Human Bcl-2 protei
c 283	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 357	20	0.4	20	22	AA15694	Human Bcl-2 protei
c 284	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 358	20	0.4	20	22	AA15695	Human Bcl-2 protei
c 285	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 359	20	0.4	20	22	AA15696	Human Bcl-2 protei
c 286	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 360	20	0.4	20	22	AA15697	Human Bcl-2 protei
c 287	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 361	20	0.4	20	22	AA15698	Human Bcl-2 protei
c 288	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 362	20	0.4	20	22	AA15699	Human Bcl-2 protei
c 289	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 363	20	0.4	20	22	AA15700	Human Bcl-2 protei
c 290	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 364	20	0.4	20	22	AA15701	Human Bcl-2 protei
c 291	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 365	20	0.4	20	22	AA15702	Human Bcl-2 protei
c 292	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 366	20	0.4	20	22	AA15703	Human Bcl-2 protei
c 293	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 367	20	0.4	20	22	AA15704	Human Bcl-2 protei
c 294	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 368	20	0.4	20	22	AA15705	Human Bcl-2 protei
c 295	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 369	20	0.4	20	22	AA15706	Human Bcl-2 protei
c 296	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 370	20	0.4	20	22	AA15707	Human Bcl-2 protei
c 297	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 371	20	0.4	20	22	AA15708	Human Bcl-2 protei
c 298	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 372	20	0.4	20	22	AA15709	Human Bcl-2 protei
c 299	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 373	20	0.4	20	22	AA15710	Human Bcl-2 protei
c 300	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 374	20	0.4	20	22	AA15711	Human Bcl-2 protei
c 301	20	0.4	20	16	AAQ86649	Human BCL2 cDNA se	c 375	20	0.4	20	22	AA15712	Human Bcl-2 protei

375	19.4	0.4	32	16	AAQ87894	Normalised library	448	19	0.4	39	18	AAQ64939	Antisense primer S
376	19.4	0.4	32	20	AAQ55013	C/EBP-beta antisen	c 449	19	0.4	39	18	AAQ65775	Repeat sequence fr
377	19.4	0.4	32	21	AAQ20582	Human C/EBP polyu	c 450	19	0.4	39	20	AAQ87088	DNA ligand T39 to
378	19.4	0.4	32	21	AAQ34460	Human adenosine re	c 451	19	0.4	39	22	AAQ21660	Immunoglobulin tra
379	19.4	0.4	32	21	AAQ98509	H. discus derived	c 452	19	0.4	40	21	AAQ05334	PCR primer bMm220r
380	19.4	0.4	33	20	AAQ55012	C/EBP-beta antisen	c 453	19	0.4	40	21	AAQ296163	Polynucleotide seq
381	19.4	0.4	33	21	AAQ20581	Human C/EBP polyu	c 454	19	0.4	40	21	AAQ43349	Murine Tyrp-1 gene
382	19.4	0.4	33	21	AAQ34459	Human adenosine re	c 455	19	0.4	40	22	AAQ20350	HHV6 virus p41 gen
383	19.4	0.4	33	22	AAQ28309	3' untranslated re	c 456	19	0.4	40	22	AAQ20354	HHV6 virus p41 gen
384	19.4	0.4	33	24	AAQ96737	Human phosphatidyl	c 457	19	0.4	40	22	AAQ38555	Human GFATL1L PCR p
385	19.4	0.4	35	16	AAQ87901	Normalised library	c 458	19	0.4	40	24	AAQ22107	Oligonucleotide 40
386	19.4	0.4	35	16	AAQ87898	Human PDE7A1 3' UT	c 459	18.8	0.4	40	24	AAQ34038	Microsatellite seq
387	19.4	0.4	36	24	AAQ33387	Normalised library	c 460	18.8	0.4	22	13	AAQ34080	Microsatellite seq
388	19.4	0.4	38	12	AAQ14795	Hepatitis C diagno	c 461	18.8	0.4	22	13	AAQ33675	Microsatellite seq
389	19.4	0.4	40	21	AAQ03676	Polynucleotide seq	c 462	18.8	0.4	22	13	AAQ33810	Microsatellite seq
390	19.4	0.4	40	21	AAQ96047	Polynucleotide seq	c 463	18.8	0.4	22	13	AAQ33991	Microsatellite seq
391	19.4	0.4	40	21	AAQ296165	Quadruplex DNA seq	c 464	18.8	0.4	22	16	AAQ83952	Oligonucleotide cl
392	19.4	0.4	40	22	AAQ57137	HHV6 virus p41 gen	c 465	18.8	0.4	22	18	AAQ65727	Repeat sequence fr
393	19.4	0.4	40	22	AAQ20347	Human bcl genes an	c 466	18.8	0.4	22	22	AAQ16448	SSR motif #8. Uni
394	18.2	0.4	20	21	AAQ65053	MC0677, a competit	c 467	18.8	0.4	22	22	AAQ16448	SSR motif #18. Uni
395	19.2	0.4	24	18	AAQ99279	Nucleotide sequenc	c 468	18.8	0.4	23	22	AAQ39005	SNP specific upper
396	19.2	0.4	24	19	AAQ31736	Oligonucleotide MC	c 469	18.8	0.4	24	18	AAQ99284	MC0677, a competit
397	19.2	0.4	24	20	AAQ04079	PCR primer specif	c 470	18.8	0.4	24	19	AAQ31741	Nucleotide sequenc
398	19.2	0.4	24	21	AAQ60156	Maize root transcr	c 471	18.8	0.4	24	20	AAQ04084	Oligonucleotide MJ
399	19.2	0.4	27	22	AAQ76445	Maize root transcr	c 472	18.8	0.4	24	20	AAQ39074	SNP specific lower
400	19.2	0.4	27	22	AAQ76448	Maize root transcr	c 473	18.8	0.4	25	15	AAQ55856	Probe for Fragile
401	18.2	0.4	27	22	AAQ26309	Triplex-forming ol	c 474	18.8	0.4	25	16	AAQ85271	Fragile X probe.
402	19.2	0.4	28	19	AAQ44665	Primer JWTCR202 us	c 475	18.8	0.4	25	20	AAQ05267	SNP specific SNPE
403	19.2	0.4	32	19	AAQ54297	Soluble sc-TCR fus	c 476	18.8	0.4	25	20	AAQ05267	SNP specific SNPE
404	19.2	0.4	32	19	AAQ54297	Antitumoural phosph	c 477	18.8	0.4	27	21	AAQ89469	Human EPIL/placent
405	19.2	0.4	34	18	AAQ93827	Reverse PCR primer	c 478	18.8	0.4	31	23	AAQ06380	Human gene signatu
406	19.2	0.4	35	16	AAQ87899	Normalised library	c 479	18.8	0.4	32	14	AAQ52007	Human inflammatory
407	19.2	0.4	35	16	AAQ87905	Normalised library	c 480	18.8	0.4	32	14	AAQ52007	Human template, AU u
408	19.2	0.4	35	18	AAQ93816	Antitumoural phosph	c 481	18.8	0.4	32	22	AAQ16452	5' PCR primer ipt
409	19.2	0.4	35	18	AAQ43757	TNFRI cytoplasmic	c 482	18.8	0.4	32	22	AAQ16452	RNA template, (AU)
410	19.2	0.4	36	18	AAQ91070	Human inflammatory	c 483	18.8	0.4	33	22	AAQ16452	Human c-myc hammer
411	19.2	0.4	37	22	AAQ85682	Pea blight resista	c 484	18.8	0.4	33	22	AAQ16452	PCR primer 2-BST-5
412	19.2	0.4	37	22	AAQ85682	Cdn primer Bclx 2-	c 485	18.8	0.4	36	22	AAQ16452	PCR primer used to
413	19.2	0.4	39	16	AAQ95496	Primer JSS33(B) us	c 486	18.8	0.4	36	22	AAQ16452	Polynucleotide seq
414	19.2	0.4	39	16	AAQ95496	BCG deletion regio	c 487	18.8	0.4	37	21	AAQ00622	Mutagenic primer A
415	19.2	0.4	40	17	AAQ33546	Polynucleotide seq	c 488	18.8	0.4	37	21	AAQ00622	Immunoglobulin tra
416	19.2	0.4	40	22	AAQ296152	HHV6 virus p41 gen	c 489	18.8	0.4	37	24	AAQ27124	Zeta globin primer
417	19.2	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym	c 490	18.8	0.4	37	24	AAQ27124	Human GDMPLP-1 25-m
418	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym	c 491	18.8	0.4	37	24	AAQ27124	Target sequence fo
419	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym	c 492	18.8	0.4	37	24	AAQ27124	Murine Zif(C7)6-Ju
420	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym	c 493	18.8	0.4	37	24	AAQ27124	supf gene triplex
421	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym	c 494	18.8	0.4	37	24	AAQ27124	
422	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym	c 495	18.8	0.4	37	24	AAQ27124	
423	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym	c 496	18.8	0.4	37	24	AAQ27124	
424	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym	c 497	18.8	0.4	37	24	AAQ27124	
425	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym	c 498	18.8	0.4	37	24	AAQ27124	
426	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym	c 499	18.8	0.4	37	24	AAQ27124	
427	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym	c 500	18.6	0.4	37	24	AAQ27124	
428	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
429	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
430	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
431	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
432	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
433	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
434	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
435	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
436	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
437	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
438	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
439	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
440	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
441	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
442	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
443	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
444	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
445	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
446	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							
447	19	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym							

ALIGNMENTS

RESULT 1
AAQ51948

ID AAQ51948 standard; RNA; 37 BP.

XX AAQ51948;

AC AAQ51948;

XX 26-MAY-1994 (first entry)

XX BCL-2 mRNA ribozyme cleavable nucleotide (1415).

XX Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
 KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
 KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
 KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
 KW human; chronic myelogenous leukemia; CML; follicular lymphoma;

KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
 KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
 KW hairpin; hepatitis delta virus; group I intron; RNaseP; ss.
 OS Homo sapiens.

XX WO9323057-A.

PN 25-NOV-1993.

XX 13-MAY-1993; 93WO-US04573.

XX 14-MAY-1992; 92US-0882822.

XX 14-MAY-1992; 92US-0882885.

XX 26-AUG-1992; 92US-0936110.

XX 26-AUG-1992; 92US-0936421.

XX 26-AUG-1992; 92US-0936422.

XX 26-AUG-1992; 92US-0936531.

XX 26-AUG-1992; 92US-0936532.

XX 07-DEC-1992; 92US-0987131.

XX 19-JAN-1993; 93US-0006122.

XX 19-JAN-1993; 93US-0008910.

XX (RIBO-) RIBOZYME PHARM INC.

XX Draper KG, Thompson JD;

XX WPI; 1993-386203/48.

XX New enzymatic RNA molecules (ribozymes) - which cleave mRNA

XX associated with tumours or mRNA expressed from gene encoding

XX multiple drug resistance

XX Claim 3; Fig 6; 69pp; English.

XX The sequences given in AAQ51825-2266 represent areas of mRNAs which are

XX associated with development or maintenance of chronic myelogenous

XX leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or

XX acute lymphocytic leukemia, follicular lymphoma, B-cell acute

XX lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma

XX and lung cancer. The full length mRNAs containing these target

XX sequences, encode aberrant cellular proteins which are able to control

XX cellular proliferation and are directly linked to a leukemic

XX phenotype. These target sequences are identified by the ribozyme of

XX the invention. The ribozymes is formed in a hammerhead motif, but may

XX also be formed in the motif of a hairpin, hepatitis delta virus, group

XX I intron or RNaseP-like RNA. These ribozymes may be used to inhibit

XX the development or expression of a transformed phenotype in man and

XX other animals by modulating expression of the corresponding gene.

XX Cleavage of target mRNAs expressed in pre-neoplastic and transformed

XX cells elicits inhibition of the transformed state. Multiple drug

XX resistance (mdr-1) mRNA specific ribozymes remove the mechanism of

XX drug resistance used by transformed cells and thus enhances drug

XX therapies for tumours. The ribozymes may also be used to study

DT

XX

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KW

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KW

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Db 1 ACCUGAACCGGCACACCGCAGGUAU 36

RESULT 3

AAX21301

ID AAX21301 standard; RNA; 36 BP.

XX AAX21301;

AC AAX21301;

XX 11-MAY-1999 (first entry)

XX Human bcl-2 mRNA as catalytic RNA substrate.

DE Cleavage; hammerhead ribozyme; catalytic RNA; gene expression; ss;

KW eukaryote; prokaryote; virus; human; tumour; plant; insect; pesticide;

KW Homo sapiens.

XX Key

XX misc_binding

XX Location/Qualifiers

XX 1..7

XX /tag= a

XX /bound_moiety= "bases 11-17 of AAX21302"

XX 9..24

XX /tag= b

XX 32..36

XX /tag= c

XX /bound_moiety= "bases 3-7 of AAX21302"

XX WO9858057-A1.

XX 23-DEC-1998.

XX 16-JUN-1998; 98WO-US12570.

XX 19-JUN-1997; 97US-0879078.

XX (INNO-) INNOVIR LAB INC.

XX Ludwig J, Sproat BS;

XX WPI; 1999-095336/08.

XX Compositions inducing cleavage of an RNA substrate - useful as drugs

XX or pesticides, and for identifying the function of a gene

XX Example 3; Fig 5A; 62pp; English.

XX The invention relates to a composition that induces cleavage of an RNA

XX substrate by forming a structure similar to a hammerhead ribozyme. This

XX sequence represents a fragment of the human bcl-2 mRNA which binds the

XX catalytic RNA AAX21302. Compositions containing catalytic RNAs can be

XX used in pharmaceutical compositions to specifically inactivate the

XX expression of genes in eukaryotes, prokaryotes and viruses, especially of

XX human genes, e.g. tumour genes or viral genes or RNA molecules in a

XX cell. They can also be used for inactivation of the expression of plant

XX or insect genes, and used as pesticides. They can be used to identify

XX the function of a gene.

XX Sequence 36 BP; 10 A; 8 C; 10 G; 8 U; 0 other;

XX Query Match

XX Best Local Similarity 0.7%; Score 36; DB 20; Length 36;

XX Matches 28; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 4147 GAAACCTGGATGTCACGGCCACTGAGGAGCTTT 4182

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

Db 1 GAAACCTGGATGTCACGGCCACTGAGGAGCTTT 36

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

RESULT 4

AAQ51966

ID AAQ51966 standard; RNA; 35 BP.

XX

AAQ51966;

XX 26-MAY-1994 (first entry)

XX BCL-2 mRNA ribozyme cleavable nucleotide (2180).

XX Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;

XX resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;

XX actinomycin D; vinblastine; small intestine; kidney; adrenal gland;

XX adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;

XX human; chronic myelogenous leukemia; CML; follicular lymphoma;

XX B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;

XX neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;

XX hairpin; hepatitis delta virus; group I intron; RNaseP; ss.

XX Homo sapiens.

XX WO9323057-A.

XX 25-NOV-1993.

XX 13-MAY-1993; 93WO-US04573.

XX 14-MAY-1992; 92US-082822.

XX 14-MAY-1992; 92US-082885.

XX 26-AUG-1992; 92US-0936110.

XX 26-AUG-1992; 92US-0936421.

XX 26-AUG-1992; 92US-0936422.

XX 26-AUG-1992; 92US-0936531.

XX 26-AUG-1992; 92US-0936532.

XX 07-DEC-1992; 92US-0987131.

XX 19-JAN-1993; 93US-0006122.

XX 19-JAN-1993; 93US-0008910.

XX (RIBO-) RIBOZYME PHARM INC.

XX Draper KG, Thompson JD;

XX WPI; 1993-386203/48.

XX New enzymatic RNA molecules (ribozymes) - which cleave mRNA

XX associated with tumours or mRNA expressed from gene encoding

XX multiple drug resistance

XX Claim 3; Fig 6; 69pp; English.

XX The sequences given in AAQ51825-2266 represent areas of mRNAs which are

XX associated with development or maintenance of chronic myelogenous

XX leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or

XX acute lymphocytic leukemia, follicular lymphoma, B-cell acute

XX lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma

XX and lung cancer. The full length mRNAs containing these target

XX sequences, encode aberrant cellular proteins which are able to control

XX cellular proliferation and are directly linked to a leukemic

XX phenotype. These target sequences are identified by the ribozyme of

XX the invention. The ribozymes is formed in a hammerhead motif, but may

XX also be formed in the motif of a hairpin, hepatitis delta virus, group

XX I intron or RNaseP-like RNA. These ribozymes may be used to inhibit

XX the development or expression of a transformed phenotype in man and

XX other animals by modulating expression of the corresponding gene.

XX Cleavage of target mRNAs expressed in pre-neoplastic and transformed

XX cells elicits inhibition of the transformed state. Multiple drug

XX resistance (mdr-1) mRNA specific ribozymes remove the mechanism of

XX drug resistance used by transformed cells and thus enhances drug

XX therapies for tumours. The ribozymes may also be used to study

XX genetic drift and mutations within cells.

XX Sequence 35 BP; 14 A; 10 C; 6 G; 5 U; 0 other;

XX Query Match

XX Best Local Similarity 0.7%; Score 35; DB 14; Length 35;

XX Matches 30; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2180 GTCAACATGCTGCCCAACAAATATGCAAAAGG 2214
J:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 GUCAACAUGCCUGCCCAACAAAUAGCAAAAGG 35

RESULT 5
AAQ86644

ID AAQ86644 standard; DNA; 35 BP.

XX AC AAQ86644;

XX DT 27-SEP-1995 (first entry)

XX DE Bcl-2 translation initiation region.

XX KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
XX KW leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;
XX KW ss.

XX OS Synthetic.

XX PN WO9508350-A.

XX PD 30-MAR-1995.

XX PF 20-SEP-1994; 94WO-US10725.

XX PR 20-SEP-1993; 93US-0124256.

XX PA (REED/) REED J C.

XX PI Reed JC;

XX DR WPI; 1995-139394/18.

XX PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
XX PT of human solid tumours, esp. breast cancer

XX PS Disclosure; Page 13; 108pp; English.

XX CC The antisense oligonucleotide TI-AS (AAQ86643) straddles the
XX CC translation-initiation site in the mRNA coding strand of the human
XX CC bcl-2 gene and is complementary to this region. It reduces the
XX CC expression of bcl-2 gene product thereby inducing programmed cell
XX CC death of certain cancer cells. The corresp. sense bcl-1 sequence
XX CC was synthesized for use as a control.

XX SQ Sequence 35 BP; 6 A; 8 C; 13 G; 8 T; 0 other;

Query Match 0.7%; Score 35; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1442 CTTTTCCTCTGGGAAGGATGGCGACGCTGGGAGA 1476

Db 1 CTTTTCCTCTGGGAAGGATGGCGACGCTGGGAGA 35

RESULT 6

AAV19652

ID AAV19652 standard; DNA; 35 BP.

XX AC AAV19652;

XX DT 12-JUN-1998 (first entry)

XX DE Human bcl-2 oligonucleotide 1.

XX KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
XX KW cancer; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN

XX US5734033-A.

XX PD 31-MAR-1998.

XX PF 24-MAR-1994; 94US-0288692.

XX PR 21-FEB-1992; 92US-0840716.

XX PR 22-DEC-1988; 88US-0288692.

XX PR 24-MAR-1994; 94US-0217082.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX PI Reed J;

XX DR WPI; 1998-229881/20.

XX PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
XX PT for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

XX PS Claim 1; Columns 3-4; 21pp; English.

XX CC This is a human bcl-2 oligonucleotide based on which an antisense
XX CC oligonucleotide complementary to the translation initiation site of the
XX CC human bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides
XX CC straddle strategic sites such as the translation initiation site, donor
XX CC and acceptor splicing sites, or sites for transportation or degradation.
XX CC Blocking translation at such strategic sites prevents the formation of a
XX CC functional bcl-2 gene product. These oligonucleotides may be used for
XX CC treating cancers associated with high levels of bcl-2 gene expression,
XX CC especially lymphomas and some leukaemias.

XX SQ Sequence 35 BP; 6 A; 8 C; 13 G; 8 T; 0 other;

Query Match 0.7%; Score 35; DB 19; Length 35;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1442 CTTTTCCTCTGGGAAGGATGGCGACGCTGGGAGA 1476

Db 1 CTTTTCCTCTGGGAAGGATGGCGACGCTGGGAGA 35

RESULT 7

ABL54150

ID ABL54150 standard; DNA; 35 BP.

XX AC ABL54150;

XX DT 12-JUL-2002 (first entry)

XX DE Bcl-2 antisense oligonucleotide.

XX KW B cell lymphoma/leukaemia-2; bcl-2; oncogene; antisense; lymphoma;
XX KW leukaemia; colon carcinoma; rectal carcinoma; pancreatic cancer;
XX KW breast cancer; ovarian cancer; prostate cancer; renal cell carcinoma;
XX KW hepatoma; bile duct carcinoma; choriocarcinoma; cervical cancer;
XX KW testicular cancer; lung carcinoma; bladder carcinoma; melanoma;
XX KW head and neck cancer; brain cancer; cytostatic; human; gene therapy;
XX KW ss.

XX OS Homo sapiens.

XX PN WO200217852-A2.

XX PD 07-MAR-2002.

XX PF 23-AUG-2001; 2001WO-US26414.

XX PR 25-AUG-2000; 2000US-227970P.

XX PR 29-SEP-2000; 2000US-237009P.

XX PR 10-NOV-2000; 2000US-0709170.

XX XX

PA (GENT-) GENTA INC.
 PI Warrel RP, Klem RE, Fingert H;
 XX WPI; 2002-371796/40.
 DR
 XX
 XX Treating or preventing cancer, tumors and carcinomas, comprises
 PT administering B cell lymphoma/leukemia-2 antisense oligonucleotide at
 PT high doses for short period for time with one or more cancer
 PT therapeutics -
 XX
 XX Disclosure; Page 53; 64pp; English.
 PS
 XX The present sequence is that of a B cell lymphoma/leukemia-2
 CC (bcl-2) antisense oligonucleotide. The present invention is
 CC directed to the use of bcl-2 antisense oligomers, particularly
 CC G3139 (see ABL54148), to treat and prevent bcl-2 related disorders.
 CC Administration at high doses results in significant therapeutic
 CC responses, including low toxicity, high tolerance and prolonged
 CC survival. Administration at high doses for short periods of time
 CC (less than 14 days) also provides significant therapeutic responses
 CC in the treatment of cancer. The bcl-2 antisense oligomer may also
 CC be used to increase the sensitivity of a subject to cancer
 CC therapeutics, and in combination with hormone treatment or gene
 CC therapy. Conditions that may be treated or prevented include
 CC cancer of the hematopoietic system, skin, bone and soft tissue,
 CC reproductive system, genitourinary system, breast, endocrine
 CC system, brain, central nervous system, peripheral nervous system,
 CC kidney, lung, respiratory system, thorax, gastrointestinal and
 CC alimentary canal, lymph nodes, pancreas, hepatobiliary system, or
 CC cancer of unknown primary site, non-Hodgkin's lymphoma, Hodgkin's
 CC lymphoma, leukemia, colon carcinoma, rectal carcinoma, pancreatic,
 CC breast, ovarian, prostate, cervical, testicular, head and neck or
 CC brain cancer, renal cell carcinoma, hepatoma, bile duct carcinoma,
 CC choriocarcinoma, lung carcinoma, bladder carcinoma and melanoma
 CC (all claimed).
 XX
 XX Sequence 35 BP; 6 A; 8 C; 13 G; 8 T; 0 other;
 SQ
 Query Match 0.7%; Score 35; DB 24; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1442 CTTTTCCTCTGGGAGGATGGCGCAGCTGGGAGA 1476
 ||||||||||||||||||||||||||||||||||||
 DB 1 CTTTTCCTCTGGGAGGATGGCGCAGCTGGGAGA 35
 RESULT 8
 AAQ51962
 ID AAQ51962 standard; RNA; 34 BP.
 XX
 XX AAQ51962;
 XX
 XX 26-MAY-1994 (first entry)
 DT
 XX BCL-2 mRNA ribozyme cleavable nucleotide (2043).
 DE
 XX Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
 KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
 KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
 KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
 KW human; chronic myelogenous leukemia; CML; follicular lymphoma;
 KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
 KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
 KW hairpin; hepatitis delta virus; group I intron; RNasep; ss.
 XX
 OS Homo sapiens.
 XX
 XX W09323057-A.
 PN
 XX
 XX 25-NOV-1993.
 PD
 XX

PF 13-MAY-1993; 93WO-US04573.
 XX
 XX 14-MAY-1992; 92US-0882822.
 PR 14-MAY-1992; 92US-0882885.
 PR 26-AUG-1992; 92US-0936110.
 PR 26-AUG-1992; 92US-0936421.
 PR 26-AUG-1992; 92US-0936422.
 PR 26-AUG-1992; 92US-0936531.
 PR 26-AUG-1992; 92US-0936532.
 PR 07-DEC-1992; 92US-0987131.
 PR 19-JAN-1993; 93US-0006122.
 PR 19-JAN-1993; 93US-0008910.
 XX
 XX (RIBO-) RIBOZYME PHARM. INC.
 PA
 XX Draper KG, Thompson JD;
 PI
 XX WPI; 1993-386203/48.
 XX
 XX New enzymatic RNA molecules (ribozymes) - which cleave mRNA
 PT associated with tumors or mRNA expressed from gene encoding
 PT multiple drug resistance
 PT
 XX Claim 3; Fig 6; 69pp; English.
 PS
 XX The sequences given in AAQ51825-2266 represent areas of mRNAs which are
 CC associated with development or maintenance of chronic myelogenous
 CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or
 CC acute lymphocytic leukemia, follicular lymphoma, B-cell acute
 CC lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma
 CC and lung cancer. The full length mRNAs containing these target
 CC sequences, encode aberrant cellular proteins which are able to control
 CC cellular proliferation and are directly linked to a leukemic
 CC phenotype. These target sequences are identified by the ribozyme of
 CC the invention. The ribozymes is formed in a hammerhead motif, but may
 CC also be formed in the motif of a hairpin, hepatitis delta virus, group
 CC I intron or RNasep-like RNA. These ribozymes may be used to inhibit
 CC the development or expression of a transformed phenotype in man and
 CC other animals by modulating expression of the corresponding gene.
 CC Cleavage of target mRNAs expressed in pre-neoplastic and transformed
 CC cells elicits inhibition of the transformed state. Multiple drug
 CC resistance (mdr-1) mRNA specific ribozymes remove the mechanism of
 CC drug resistance used by transformed cells and thus enhances drug
 CC therapies for tumors. The ribozymes may also be used to study
 CC genetic drift and mutations within cells.
 XX
 XX Sequence 34 BP; 6 A; 9 C; 11 G; 8 U; 0 other;
 SQ
 Query Match 0.7%; Score 34; DB 14; Length 34;
 Best Local Similarity 76.5%; Pred. No. 5.2e+02;
 Matches 26; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
 OY 2043 GGATGCCCTTTGTGGAACTGTACGGCCCCCAGCATG 2076
 |||:||||:||||:||||:||||:||||:|
 DB 1 GGAUGCCUUUGUGGAACUGACGGCCCCCAGCAUG 34
 RESULT 9
 AAQ51967
 ID AAQ51967 standard; RNA; 34 BP.
 XX
 XX AAQ51967;
 AC
 XX
 XX 26-MAY-1994 (first entry)
 DT
 XX BCL-2 mRNA ribozyme cleavable nucleotide (2235).
 DE
 XX Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
 KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
 KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
 KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
 KW human; chronic myelogenous leukemia; CML; follicular lymphoma;
 KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
 KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
 KW hairpin; hepatitis delta virus; group I intron; RNasep; ss.
 XX
 OS Homo sapiens.
 XX
 XX W09323057-A.
 PN
 XX
 XX 25-NOV-1993.
 PD
 XX


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RESULT 12
AAD12893/c
ID AAD12893 standard; RNA; 36 BP.
XX AC AAD12893;
XX AC AAD12894;
XX DT 16-OCT-2001 (first entry)
XX DE Anti-sense RNA targetted to bcl-2-IgH fusion gene.
XX DE Human; double stranded RNA dependent protein kinase; PKR; genetic locus;
XX KW antisense; therapy; proliferative disorder; neoplastic disease;
XX KW psoriasis; vasculogenesis; angiogenesis; apoptosis; cytostatic; bcl-2;
XX KW immunoglobulin heavy chain; IgH; fusion protein; DCLL;
XX KW follicular lymphoma; FT; chromosomal translocation; ss.
XX OS Homo sapiens.
XX PN WO200157205-A1.
XX PD 09-AUG-2001.
XX PF 31-JAN-2001; 2001WO-IL00094.
XX PR 31-JAN-2000; 2000US-0179361.
XX PR 22-DEC-2000; 2000US-0258010.
XX PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX PI Shir A, Levitzky A;
XX WPI; 2001-488878/53.
XX PT Activating double stranded RNA dependent protein kinase in targeted
XX PT cell population, by hybridizing antisense RNA with sequence at single
XX PT genetic locus in the population, that is absent in non-targeted
XX PT population -
XX PS Claim 30; Page 12; 54pp; English.
XX CC The present invention relates to a method for selective killing of cells
XX CC in a targeted cell population by selectively activating double stranded
XX CC (ds) RNA dependent protein kinase (PKR). The method involves selecting
XX CC sequence at single genetic locus in targeted cell population that is
XX CC absent from equivalent locus in non-targeted cell population, obtaining
XX CC anti-sense RNA having sequence homology with the genetic locus, and
XX CC permitting anti-sense RNA to hybridise with the RNA transcribed from the
XX CC genetic locus to form contiguous dsRNA for activating PKR. The method is
XX CC also used for treating proliferative disorders such as neoplastic
XX CC disease, psoriasis and vasculogenesis or angiogenesis. The present
XX CC sequence is an anti-sense RNA targetted to antiapoptotic
XX CC bcl-2-immunoglobulin heavy chain (IgH) locus fusion gene. The DCLL and
XX CC follicular lymphoma (FT) is characterised by a t(14;18)(q32;q21)
XX CC chromosomal translocation of bcl-2-IgH fusion gene.
XX SQ Sequence 36 BP; 7 A; 11 C; 3 G; 15 U; 0 other;
Query Match 0.6%; Score 31.2; DB 22; Length 36;
Best Local Similarity 91.7%; Pred. No. 2.2e+03;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4098 CAAAGCATTTCTGAGAGGTTGAGATAGCCCTGAGT 4133
DB 36 CAAAGGATTTCTGAGAGGTTGAGATAGAACTGAGT 1
RESULT 13
AAD12894
ID AAD12894 standard; DNA; 30 BP.
XX AC AAD12894;
XX DT 27-MAY-1997 (first entry)
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RESULT 11
AAD12894
ID AAD12894 standard; DNA; 36 BP.
XX AC AAD12894;
XX DT 16-OCT-2001 (first entry)
XX DE Bcl-2-IgH fusion gene comprising chromosomal translocation t(14;18).
XX DE Human; double stranded RNA dependent protein kinase; PKR; genetic locus;
XX KW antisense; therapy; proliferative disorder; neoplastic disease;
XX KW psoriasis; vasculogenesis; angiogenesis; apoptosis; cytostatic; bcl-2;
XX KW immunoglobulin heavy chain; IgH; fusion protein; DCLL;
XX KW follicular lymphoma; FT; chromosomal translocation; ds.
XX OS Homo sapiens.
XX PN WO200157205-A1.
XX PD 09-AUG-2001.
XX PF 31-JAN-2001; 2001WO-IL00094.
XX PR 31-JAN-2000; 2000US-0179361.
XX PR 22-DEC-2000; 2000US-0258010.
XX PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX PI Shir A, Levitzky A;
XX WPI; 2001-488878/53.
XX PT Activating double stranded RNA dependent protein kinase in targeted
XX PT cell population, by hybridizing antisense RNA with sequence at single
XX PT genetic locus in the population, that is absent in non-targeted
XX PT population -
XX PS Disclosure; Page 12; 54pp; English.
XX CC The present invention relates to a method for selective killing of cells
XX CC in a targeted cell population by selectively activating double stranded
XX CC (ds) RNA dependent protein kinase (PKR). The method involves selecting
XX CC sequence at single genetic locus in targeted cell population that is
XX CC absent from equivalent locus in non-targeted cell population, obtaining
XX CC anti-sense RNA having sequence homology with the genetic locus, and
XX CC permitting anti-sense RNA to hybridise with the RNA transcribed from the
XX CC genetic locus to form contiguous dsRNA for activating PKR. The method is
XX CC also used for treating proliferative disorders such as neoplastic
XX CC disease, psoriasis and vasculogenesis or angiogenesis. The present
XX CC sequence is an antiapoptotic bcl-2-immunoglobulin heavy chain (IgH) locus
XX CC fusion gene comprising chromosomal translocation t(14;18)(q32;q21). The
XX CC DCLL and follicular lymphoma (FT) is characterised by the chromosomal
XX CC translocation of bcl-2-IgH fusion gene.
XX SQ Sequence 36 BP; 15 A; 4 C; 10 G; 7 T; 0 other;
Query Match 0.6%; Score 32.8; DB 22; Length 36;
Best Local Similarity 94.4%; Pred. No. 9.7e+02;
Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4098 CAAAGCATTTCTGAGAGGTTGAGATAGCCCTGAGT 4133
DB 1 CAAAGGATTTCTGAGAGGTTGAGATAGAACTGAGT 36
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XX DE Non-Hodgkin's B cell line bcl-2/IgH chimeric gene PCR primer.
XX KW Non-Hodgkin's lymphoma; cell line DOHH2; DHL-4; leukaemia; chromosome;
XX KW t14; t18; q21; q21; N region; antisense; expression; inhibitor;
XX KW bcl-2; IgH; immunoglobulin heavy chain; hybrid; cell death; tumour;
XX KW cancer; neoplasia; diagnosis; translocation; chimera; PCR;
XX KW polymerase chain reaction; ss.
XX OS Synthetic.
XX XX
XX PN WO9627663-A2.
XX XX
XX PD 12-SEP-1996.
XX XX
XX PF 02-MAR-1996; 96WO-EP00852.
XX XX
XX PR 03-MAR-1995; 95IT-OMI0420.
XX XX
XX PA (CNDR ) CONSIGLIO NAZ DELLE RICERCHE.
XX PI Capaccioli S, Morelli S, Nicolin A;
XX DR WPI; 1996-425424/42.
XX XX
XX PT New chimeric bcl-2/IgH antisense transcript of t(14; 18)
XX PT translocated cells - used to develop oligodeoxynucleotides for the
XX PT diagnosis and treatment of tumours associated with the
XX PT translocation.
XX PS Example 1; Page 11; 32pp; English.
XX XX
XX CC AAT35441-T35443 are PCR primers used to amplify the chimeric bcl-2/IgH
XX CC (immunoglobulin heavy chain) gene present in the t(14; 18) chromosomally
XX CC translocated non-Hodgkin's lymphoma cell line DOHH-2. The transcript
XX CC produced is used for the design of antisense transcripts which can
XX CC inhibit the production of bcl-2 protein in t(14; 18) translocated cells
XX CC and induce cell death. The antisense transcripts can be used for the
XX CC diagnosis and treatment of t(14; 18)-associated tumours and for
XX CC monitoring treatment of a pathology associated with a t(14; 18)
XX CC translocation.
XX SQ Sequence 30 BP; 3 A; 9 C; 6 G; 12 T; 0 other;

Query Match 0.6%; Score 30; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4256 GACCTGTGTTCTGAAGGTTCTCTGTCCTCC 4285
DB 1 GACCTGTGTTCTGAAGGTTCTCTGTCCTCC 30

RESULT 14
AAT66066
ID AAT66066 standard; DNA; 30 BP.
XX AC AAT66066;
XX XX
XX DT 18-JUN-1997 (first entry)
XX DE (dC-dA)n.(dG-dT)n polymorphic repeat sequence #7.
XX XX
XX KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
XX KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
XX KW linkage analysis; genetic disease; animal; plant; breeding; locus;
XX KW hybridisation; chromosome; ds.
XX OS Homo sapiens.
XX XX
XX PN US5582979-A.
XX XX
XX PD 10-DEC-1996.

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XX PF 21-APR-1989; 89US-0341562.
XX PR 05-SEP-1991; 91US-0754351.
XX PR 21-APR-1989; 89US-0341562.
XX PR 04-APR-1994; 94US-0222177.
XX XX
XX PA (MARS-) MARSHFIELD CLINIC.
XX XX
XX PI Weber JL;
XX PT WPI; 1997-042299/04.
XX DR Detection of polymorphic genetic markers of the form
XX PT (dC-dA)n(dG-dT)n - using novel nucleic acid mois. as primers
XX XX
XX PS Example 8; Column 57-58; 186pp; English.
XX XX
XX CC The invention relates to the isolation of polymorphic repeat sequences
XX CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
XX CC markers. Primers based on these sequences can be used to detect these
XX CC repeats, especially for use in e.g. paternity or maternity testing,
XX CC human genetic analysis such as linkage analysis of genetic disease,
XX CC commercial animal or plant breeding or pedigree analysis.
XX CC The repeats, when analysed, fall into 4 categories:
XX CC 1) perfect repeats which are alternating tandem CA repeats with no
XX CC interruptions and without adjacent repeats of another sequence;
XX CC 2) imperfect repeats which are defined as 2 or more runs of uninterrupted
XX CC CA repeats separated by no more than 3 consecutive non-repeat bases;
XX CC 3) compound perfect repeats which are uninterrupted runs of CA separated
XX CC by no more than 3 consecutive non-repeat bases from a run of at least
XX CC 5 uninterrupted dinucleotide or longer repeats of a sequence other than
XX CC (dC-dA)n.(dG-dT)n, or from at least 10 uninterrupted mononucleotides; and
XX CC 4) imperfect compound repeats which are defined as for the perfect
XX CC compound repeats except that the runs of CA are interrupted.
XX CC This sequence is an example of an imperfect repeat sequence of structure:
XX CC (CA)5G(ACA)G(AC)7A.
XX XX
XX SQ Sequence 30 BP; 15 A; 13 C; 2 G; 0 U; 0 other;

Query Match 0.6%; Score 30; DB 18; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACACA 2339
DB 1 CACACACACACACACACACACACACACACA 30

RESULT 15
AAQ68850
ID AAQ68850 standard; DNA; 38 BP.
XX AC AAQ68850;
XX XX
XX DT 28-OCT-1994 (first entry)
XX DE Human chromosomal repeat element.
XX XX
XX KW Yeast Artificial Chromosome; YAC; polymerase chain reaction; PCR;
XX KW sequence tagged site; genetic disorder; diagnosis; abnormality;
XX KW Prader-Willi; Angelman; Beckwith-Wiedemann; syndrome; ds.
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT repeat_region 5..38 /*tag= a
XX FT /*tag= b
XX FT repeat_unit 5..6
XX FT /*tag= b
XX XX
XX PN WO9406936-A.

```


XX PI Capaccioli S, Morelli S, Nicolin A;
 XX DR WPI; 1996-425424/42.
 XX PT New chimeric bcl-2/IgH antisense transcript of t(14; 18)
 PT translocated cells - used to develop oligodeoxynucleotides for the
 PT diagnosis and treatment of tumours associated with the
 XX translocation.
 XX PS Example 1; Page 12; 32pp; English.
 XX CC AAT35441-T35443 are PCR primers used to amplify the chimeric bcl-2/IgH
 CC (immunoglobulin heavy chain) gene present in the t(14; 18) chromosomally
 CC translocated non-Hodgkin's lymphoma cell line DOHH-2. The transcript
 CC produced is used for the design of antisense transcripts which can
 CC inhibit the production of bcl-2 protein in t(14; 18) translocated cells
 CC and induce cell death. The antisense transcripts can be used for the
 CC diagnosis and treatment of t(14; 18)-associated tumours and for
 CC monitoring treatment of a pathology associated with a t(14; 18)
 CC translocation.
 XX Sequence 30 BP; 9 A; 9 C; 7 G; 5 T; 0 other;
 XX
 XX Query Match 0.6%; Score 28; DB 17; Length 30;
 XX Best Local Similarity 100.0%; Pred. No. 1e+04;
 XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 4504 CTTGAGGCTCTCTGAAATGCAGTGGT 4531
 DB 30 CTTGAGGCTCTCTGAAATGCAGTGGT 3
 RESULT 18
 AAT35446/C
 ID AAT35446 standard; DNA; 30 BP.
 XX AC AAT35446;
 XX DT 27-MAY-1997 (first entry)
 XX DE Non-Hodgkin's B cell line bcl-2/IgH chimeric gene PCR primer.
 XX KW Non-Hodgkin's lymphoma; cell line DOHH2; DHL-4; leukaemia; chromosome;
 KW t14; t18; q32; q21; N region; antisense; expression; inhibitor;
 KW bcl-2; IgH; immunoglobulin heavy chain; hybrid; cell death; tumour;
 KW cancer; neoplasia; diagnosis; translocation; chimera; PCR;
 KW polymerase chain reaction; ss.
 XX Synthetic.
 XX WO9627663-A2.
 XX PD 12-SEP-1996.
 XX PF 02-MAR-1996; 96WO-EP00852.
 XX PR 03-MAR-1995; 95IT-OMI0420.
 XX PA (CNR) CONSIGLIO NAZ DELLE RICERCHE.
 XX PI Capaccioli S, Morelli S, Nicolin A;
 XX DR WPI; 1996-425424/42.
 XX PT New chimeric bcl-2/IgH antisense transcript of t(14; 18)
 PT translocated cells - used to develop oligodeoxynucleotides for the
 PT diagnosis and treatment of tumours associated with the
 XX translocation.
 XX PS Example 1; Page 12; 32pp; English.
 XX CC AAT35446 and AAT35447 are PCR primers used to amplify the chimeric
 CC bcl-2/IgH (immunoglobulin heavy chain) gene present in the t(14; 18)
 CC chromosomally translocated non-Hodgkin's lymphoma cell line DOHH-2. The
 CC primers correspond to the 3' untranslated region of the bcl-2 gene. The
 CC transcript produced is used for the design of antisense transcripts
 CC which can inhibit the production of bcl-2 protein in t(14; 18)
 CC translocated cells and induce cell death. The antisense transcripts can
 CC be used for the diagnosis and treatment of t(14; 18)-associated tumours
 CC and for monitoring treatment of a pathology associated with a t(14; 18)
 CC translocation.

CC bcl-2/IgH (immunoglobulin heavy chain) gene present in the t(14; 18)
 CC chromosomally translocated non-Hodgkin's lymphoma cell line DOHH-2. The
 CC primers correspond to the 3' untranslated region of the bcl-2 gene. The
 CC transcript produced is used for the design of antisense transcripts
 CC which can inhibit the production of bcl-2 protein in t(14; 18)
 CC translocated cells and induce cell death. The antisense transcripts can
 CC be used for the diagnosis and treatment of t(14; 18)-associated tumours
 CC and for monitoring treatment of a pathology associated with a t(14; 18)
 CC translocation.
 XX Sequence 30 BP; 9 A; 9 C; 7 G; 5 T; 0 other;
 XX
 XX Query Match 0.6%; Score 28; DB 17; Length 30;
 XX Best Local Similarity 100.0%; Pred. No. 1e+04;
 XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 4504 CTTGAGGCTCTCTGAAATGCAGTGGT 4531
 DB 30 CTTGAGGCTCTCTGAAATGCAGTGGT 3
 RESULT 19
 AAT35447/C
 ID AAT35447 standard; DNA; 30 BP.
 XX AC AAT35447;
 XX DT 27-MAY-1997 (first entry)
 XX DE Non-Hodgkin's B cell line bcl-2/IgH chimeric gene PCR primer.
 XX KW Non-Hodgkin's lymphoma; cell line DOHH2; DHL-4; leukaemia; chromosome;
 KW t14; t18; q32; q21; N region; antisense; expression; inhibitor;
 KW bcl-2; IgH; immunoglobulin heavy chain; hybrid; cell death; tumour;
 KW cancer; neoplasia; diagnosis; translocation; chimera; PCR;
 KW polymerase chain reaction; ss.
 XX Synthetic.
 XX WO9627663-A2.
 XX PD 12-SEP-1996.
 XX PF 02-MAR-1996; 96WO-EP00852.
 XX PR 03-MAR-1995; 95IT-OMI0420.
 XX PA (CNR) CONSIGLIO NAZ DELLE RICERCHE.
 XX PI Capaccioli S, Morelli S, Nicolin A;
 XX DR WPI; 1996-425424/42.
 XX PT New chimeric bcl-2/IgH antisense transcript of t(14; 18)
 PT translocated cells - used to develop oligodeoxynucleotides for the
 PT diagnosis and treatment of tumours associated with the
 XX translocation.
 XX PS Example 1; Page 12; 32pp; English.
 XX CC AAT35446 and AAT35447 are PCR primers used to amplify the chimeric
 CC bcl-2/IgH (immunoglobulin heavy chain) gene present in the t(14; 18)
 CC chromosomally translocated non-Hodgkin's lymphoma cell line DOHH-2. The
 CC primers correspond to the 3' untranslated region of the bcl-2 gene. The
 CC transcript produced is used for the design of antisense transcripts
 CC which can inhibit the production of bcl-2 protein in t(14; 18)
 CC translocated cells and induce cell death. The antisense transcripts can
 CC be used for the diagnosis and treatment of t(14; 18)-associated tumours
 CC and for monitoring treatment of a pathology associated with a t(14; 18)
 CC translocation.
 XX Sequence 30 BP; 9 A; 9 C; 7 G; 5 T; 0 other;

Query Match 0.6%; Score 28; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4504 CTTGAGGCTCTCTGAAATCAGTGGT 4531
 |||||
 Db 30 CTTGAGGCTCTCTGAAATCAGTGGT 3

RESULT 20
 AAH45307
 ID AAH45307 standard; DNA; 36 BP.
 XX
 AC AAH45307;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 SE Human Bcl-2 PCR primer oligo-10.
 XX
 NM Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200142459-A1.
 XX
 PD 14-JUN-2001.
 XX
 PF 07-DEC-2000; 2000WO-JP08667.
 XX
 PR 09-DEC-1999; 99JP-0350427.
 XX
 PA (HISM) HISAMITSU PHARM CO LTD.
 XX
 PI Shibazaki F, Kuma H;
 XX
 XX WPI; 2001-381681/40.
 DR
 XX
 PT New apoptosis inhibitors, useful for treating apoptosis related
 disorders -
 XX
 PS Example 1; Page 39; 43pp; Japanese.
 XX
 CC The invention relates to an apoptosis inhibitor comprising the
 CC amino acid sequence of Bcl-2 protein in which at least one serine
 CC residue is substituted by alanine or aspartic acid. The protein has
 CC increased apoptosis inhibitory activity compared with the wild type
 CC Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment
 CC of disorders caused by apoptosis. The present sequence was used to
 CC amplify DNA encoding the human Bcl-2 protein.
 XX
 SQ Sequence 36 BP; 7 A; 10 C; 15 G; 4 T; 0 other;

Query Match 0.6%; Score 28; DB 22; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1458 GATGGCGCACGCTGGGAGACGGGTAC 1485
 |||||
 Db 9 GATGGCGCACGCTGGGAGACGGGTAC 36

RESULT 21
 AAZ98493
 ID AAZ98493 standard; DNA; 40 BP.
 XX
 AC AAZ98493;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE H. discus derived sequence #11.
 XX
 KW Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
 KW Halliotis discus; ss.

XX Halliotis discus.
 OS WO200011156-A1.
 PN 02-MAR-2000.
 XX
 PD 01-JUL-1999; 99WO-JP03551.
 XX
 PF 18-AUG-1998; 98JP-0232153.
 XX
 PR (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
 XX
 PA Takahashi H, Sekino M;
 XX
 PI WPI; 2000-224692/19.
 DR
 XX
 SE Isolation of satellite sequences from genomic DNA for use as DNA
 XX markers comprises isolating a library with high homogeneity by DNA
 PT fragmentation -
 PT
 XX Example 5; Page 14; 35pp; Japanese.
 PS
 XX The invention provides a novel method for isolation of satellite
 CC sequences from genomic DNA that comprises fragmentation of the DNA by
 CC a method which is not dependent on base sequences, then selection of
 CC the satellite sequences from the obtained genomic library of high
 CC homogeneity. The method is useful for the isolation of microsatellite
 CC DNA sequences which can be used as DNA markers. The new method markedly
 CC improves the efficiency of isolation of satellite sequences in
 CC comparison to prior art methods which are reliant on base sequences.
 CC Sequences AAZ98483-514 represent sequences from Halliotis discus, used in
 CC the method of the invention.
 XX
 SQ Sequence 40 BP; 19 A; 19 C; 0 G; 2 T; 0 other;

Query Match 0.5%; Score 27.8; DB 21; Length 40;
 Best Local Similarity 93.5%; Pred. No. 1.2e+04;
 Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2309 TCACACACACACACACACACACACACACA 2339
 |||||
 Db 4 TCACACACACACACACACACACACACACA 34

RESULT 22
 AAQ33894/C
 ID AAQ33894 standard; DNA; 38 BP.
 XX
 AC AAQ33894;
 XX
 DT 02-FEB-1993 (first entry)
 XX
 DE Microsatellite sequence from clone TGLA309.
 XX
 KW PCR; selection; primers; OPTIPRM; breeding; cattle; parentage;
 XX genetic mapping; traits; amplification; ss.
 XX
 OS Bos taurus.
 XX
 PN WO9213102-A.
 XX
 PD 06-AUG-1992.
 XX
 PF 15-JAN-1992; 92WO-US00340.
 XX
 PR 15-JAN-1991; 91US-0642342.
 XX
 PA (GENM-) GENMARK.
 XX
 PI Georges M, Massey JM;
 XX
 XX WPI; 1992-284684/34.

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The sequence is that of a bovine microsatellite sequence obtd. by
 screening a library of bovine MboI DNA fragments of between
 250 and 500 bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe.
 One out of 50 clones cross-hybridised. Assuming independent
 distribution of microsatellites and MboI sites, the frequency of
 (76)n > 9 microsatellites in the bovine genome is estimated at >100,
 000. The sequence information for ca. 230 such bovine microsatellites
 is summarised in the specification and indexed herein (see below).
 The sequences upstream and downstream of the microsatellite sequence
 were used to generate the required PCR primers for in vitro

KW hybridisation; chromosome; ds.

XX Homo sapiens.

XX US5582979-A.

XX 10-DEC-1996.

XX 21-APR-1989; 89US-0341562.

XX 05-SEP-1991; 91US-0754351.

XX 21-APR-1989; 89US-0341562.

XX 04-APR-1994; 94US-0222177.

XX (MARS-) MARSHFIELD CLINIC.

XX Weber JL;

XX WPI; 1997-042299/04.

XX Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers

XX Disclosure; Column 11-12; 186pp; English.

XX The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g. paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-R66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf64 which contains the repeat sequence having the formula: (AC)15.5.

XX Sequence 31 BP; 16 A; 15 C; 0 G; 0 U; 0 other;

XX Query Match 0.5%; Score 26.8; DB 18; Length 31;

XX Best Local Similarity 93.3%; Pred. No. 1.9e+04;

XX Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 2310 CACACACACACACACACACACACACA 2339

XX 2 CACACACACACACACACACACACACA 31

XX RESULT 41

XX AAQ33666/C

XX ID AAQ33666 standard; DNA; 32 BP.

XX AC AAQ33666;

XX 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone TGLA111.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX WO9213102-A.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US00340.

XX 15-JAN-1991; 91US-0642342.

XX

PA (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding

XX Table 7; Page 196; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites in the bovine genome is estimated at >100,000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved in the determination of economically important traits esp. in cattle, to allow selective breeding.

XX See also AAQ33501-34437.

XX Sequence 32 BP; 0 A; 0 C; 16 G; 16 T; 0 other;

XX Query Match 0.5%; Score 26.8; DB 13; Length 32;

XX Best Local Similarity 93.3%; Pred. No. 1.9e+04;

XX Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 2310 CACACACACACACACACACACACACA 2339

XX 31 CACACACACACACACACACACACACA 2

XX RESULT 42

XX AAT65790

XX ID AAT65790 standard; DNA; 32 BP.

XX AC AAT65790;

XX 17-JUN-1997 (first entry)

XX Repeat sequence from polymorphic marker clone Mfd119.

XX Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.

XX Homo sapiens.

XX US5582979-A.

XX 10-DEC-1996.

XX 21-APR-1989; 89US-0341562.

XX 05-SEP-1991; 91US-0754351.

XX 21-APR-1989; 89US-0341562.

XX 04-APR-1994; 94US-0222177.

XX (MARS-) MARSHFIELD CLINIC.

XX Weber JL;

XX WPI; 1997-042299/04.

XX Detection of polymorphic genetic markers of the form

XX

The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)_n, (dG-dT)_n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g. paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones

The present invention describes an isolated nucleotide sequence (1) encoding at least a portion of the human alpha-7 neuronal nicotinic acetylcholine receptor (alpha7-hnAChR). Also described are: (1) a peptide encoded by (1); (2) a vector comprising (1); (3) a host cell transformed with a vector of (2); (4) a polynucleotide comprising at least 15 nucleotides which hybridises under stringent conditions to a least a portion of (1); (5) a method for detection of a polynucleotide encoding alpha 7-hnAChR in a biological sample; and (6) a method for amplification of nucleic acid from a sample suspected of containing nucleic acid encoding alpha 7-hnAChR. The primers and probes from the present invention can be used on brain tissue and blood samples of humans suspected of suffering from schizophrenia, small cell lung carcinoma, breast cancer and nicotine-dependent illness. This is particularly useful for diagnosis of schizophrenia. Other illnesses that can be studied/diagnosed are epilepsy (e.g. juvenile myoclonic

XX PN US582979-A.
 XX XX
 XX PD 10-DEC-1996.
 XX XX
 XX PF 21-APR-1989; 89US-0341562.
 XX XX
 XX PR 05-SEP-1991; 91US-0754351.
 XX PR 21-APR-1989; 89US-0341562.
 XX PR 04-APR-1994; 94US-0222177.
 XX XX
 XX PA (MARS-) MARSHFIELD CLINIC.
 XX XX
 XX PI Weber JL;
 XX XX
 XX DR WPI; 1997-042299/04.
 XX XX
 XX PT Detection of polymorphic genetic markers of the form
 XX PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
 XX PS
 XX PS Claim 1; Column 9-10; 186pp; English.
 XX XX
 XX CC The invention relates to the isolation of polymorphic repeat sequences
 XX CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
 XX CC markers. Primers based on these sequences can be used to detect these
 XX CC repeats, especially for use in e.g. paternity or maternity testing,
 XX CC human genetic analysis such as linkage analysis of genetic disease,
 XX CC commercial animal or plant breeding or pedigree analysis. Clones
 XX CC containing the repeat sequences were isolated by hybridisation of
 XX CC chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
 XX CC probe. Over 100 repeat blocks were isolated. The inserts from the
 XX CC clones were amplified by primers AAT65798-T66047. Those clones where the
 XX CC repeat sequence has been determined are shown in AAT65704-797. This
 XX CC repeat sequence is from the marker clone Mdf3 which contains the repeat
 XX CC sequence having the formula: (CA)16C.
 XX XX
 XX SQ Sequence 33 BP; 16 A; 17 C; 0 G; 0 U; 0 other;
 XX XX
 XX Query Match 0.5%; Score 26.8; DB 18; Length 33;
 XX Best Local Similarity 93.3%; Pred. No. 1.9e+04;
 XX Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX XX
 XX QY 2310 CACACACACACACACACACACACACACA 2339
 XX Db ||||||||| ||| ||||||||| |||||
 XX 1 CACACACACACACACACACACACACACA 30
 XX XX
 XX RESULT 50
 XX AAT65754
 XX ID AAT65754 standard; DNA; 33 BP.
 XX XX
 XX AC AAT65754;
 XX XX
 XX DT 17-JUN-1997 (first entry)
 XX XX
 XX DE Repeat sequence from polymorphic marker clone Mfd58.
 XX XX
 XX KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
 XX KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
 XX KW linkage analysis; genetic disease; animal; plant; breeding; locus;
 XX KW hybridisation; chromosome; ds.
 XX XX
 XX OS Homo sapiens.
 XX XX
 XX PN US582979-A.
 XX XX
 XX PD 10-DEC-1996.
 XX XX
 XX PF 21-APR-1989; 89US-0341562.
 XX XX
 XX PR 05-SEP-1991; 91US-0754351.
 XX PR 21-APR-1989; 89US-0341562.
 XX PR 04-APR-1994; 94US-0222177.
 XX PR

XX (MARS-) MARSHFIELD CLINIC.
 XX Weber JL;
 XX WPI; 1997-042299/04.
 XX Detection of polymorphic genetic markers of the form
 XX (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
 XX Disclosure; Column 11-12; 186pp; English.
 XX XX
 XX CC The invention relates to the isolation of polymorphic repeat sequences
 XX CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
 XX CC markers. Primers based on these sequences can be used to detect these
 XX CC repeats, especially for use in e.g. paternity or maternity testing,
 XX CC human genetic analysis such as linkage analysis of genetic disease,
 XX CC commercial animal or plant breeding or pedigree analysis. Clones
 XX CC containing the repeat sequences were isolated by hybridisation of
 XX CC chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
 XX CC probe. Over 100 repeat blocks were isolated. The inserts from the
 XX CC clones were amplified by primers AAT65798-T66047. Those clones where the
 XX CC repeat sequence has been determined are shown in AAT65704-797. This
 XX CC repeat sequence is from the marker clone Mdf58 which contains the repeat
 XX CC sequence having the formula: (CA)16.5.
 XX XX
 XX SQ Sequence 33 BP; 16 A; 17 C; 0 G; 0 U; 0 other;
 XX XX
 XX Query Match 0.5%; Score 26.8; DB 18; Length 33;
 XX Best Local Similarity 93.3%; Pred. No. 1.9e+04;
 XX Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX XX
 XX QY 2310 CACACACACACACACACACACACACACA 2339
 XX Db ||||||||| ||| ||||||||| |||||
 XX 1 CACACACACACACACACACACACACACA 30
 XX XX
 XX Search completed: May 31, 2003, 16:59:59
 XX Job time : 1020 secs

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OM nucleic - nucleic search, using sw model

Run on: May 31, 2003, 16:41:01 ; Search time 610 Seconds
(without alignments) 11242.271 Million cells

Title: US-09-375-514-19
Perfect score: 5086
Sequence: 1 aacccccccccctccc

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 845702 seqs, 674182571 residues
Total number of hits satisfying chosen parameters: 471460

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Minimum DB seq length: 10
Maximum DB seq length: 40
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

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14: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
C 1	26.8	0.5	31	9	US-10-085-906-27	Sequence 27, Appl
C 2	26.8	0.5	39	10	US-09-263-959-678	Sequence 678, App
C 3	25.8	0.5	30	9	US-10-085-906-93	Sequence 93, Appl
C 4	25.2	0.5	34	10	US-09-263-959-711	Sequence 711, App
C 5	24.2	0.5	29	10	US-09-263-959-665	Sequence 665, App
C 6	24	0.5	24	10	US-09-920-342-9	Sequence 9, Appl
C 7	24	0.5	24	10	US-09-920-342-11	Sequence 11, Appl
C 8	23.8	0.5	27	10	US-09-735-363A-1	Sequence 1, Appl
C 9	23.8	0.5	27	10	US-09-735-363A-5	Sequence 5, Appl
C 10	23.8	0.5	27	10	US-09-735-363A-56	Sequence 66, Appl
C 11	23.8	0.5	27	10	US-09-263-959-770	Sequence 770, App
C 12	23.6	0.5	30	10	US-09-263-959-600	Sequence 600, App
C 13	22.4	0.4	24	9	US-09-970-820-11	Sequence 11, Appl
C 14	22.4	0.4	24	9	US-09-986-718-11	Sequence 11, Appl
C 15	22.4	0.4	24	10	US-09-371-900-11	Sequence 11, Appl
C 16	22	0.4	22	9	US-09-931-732-21	Sequence 21, Appl
C 17	21.4	0.4	33	10	US-09-925-674A-1	Sequence 1, Appl
C 18	21.2	0.4	39	9	US-10-231-381-27	Sequence 27, Appl
C 19	21	0.4	31	10	US-09-925-674A-3	Sequence 3, Appl

c 93	18	0.4	18	9	US-09-835-370-21	Sequence 21, Appl	166	17.6	0.3	24	9	US-10-035-958-19	Sequence 19, Appl
c 94	18	0.4	18	9	US-09-888-326-755	Sequence 755, Appl	167	17.6	0.3	24	9	US-10-036-150-19	Sequence 19, Appl
c 95	18	0.4	18	9	US-09-888-326-756	Sequence 756, Appl	168	17.6	0.3	24	9	US-10-036-150-19	Sequence 19, Appl
c 96	18	0.4	18	9	US-09-931-732-20	Sequence 20, Appl	169	17.6	0.3	24	12	US-10-036-342-19	Sequence 19, Appl
c 97	18	0.4	18	9	US-09-818-918-55	Sequence 55, Appl	170	17.6	0.3	25	9	US-10-060-830-506	Sequence 506, Appl
c 98	18	0.4	18	9	US-10-112-653-1	Sequence 1, Appl	171	17.6	0.3	25	9	US-10-060-830-506	Sequence 506, Appl
c 99	18	0.4	18	9	US-10-112-653-85	Sequence 85, Appl	c 172	17.6	0.3	25	10	US-09-866-108-3882	Sequence 3882, Ap
c 100	18	0.4	18	9	US-10-017-995-1	Sequence 1, Appl	c 173	17.6	0.3	25	10	US-09-866-108-3884	Sequence 3884, Ap
c 101	18	0.4	18	9	US-10-017-995-54	Sequence 54, Appl	174	17.6	0.3	30	10	US-09-725-720-25	Sequence 25, Appl
c 102	18	0.4	18	9	US-10-017-995-55	Sequence 55, Appl	175	17.6	0.3	31	10	US-09-801-274-399	Sequence 399, App
c 103	18	0.4	18	9	US-10-017-995-91	Sequence 91, Appl	176	17.6	0.3	33	10	US-09-263-959-825	Sequence 825, App
c 104	18	0.4	18	9	US-09-776-479-1	Sequence 1, Appl	177	17.6	0.3	34	9	US-09-769-787-383	Sequence 383, App
c 105	18	0.4	18	9	US-09-776-479-54	Sequence 54, Appl	178	17.6	0.3	35	9	US-10-012-896-815	Sequence 815, App
c 106	18	0.4	18	9	US-09-776-479-55	Sequence 55, Appl	179	17.6	0.3	35	9	US-09-895-793-815	Sequence 815, App
c 107	18	0.4	18	9	US-09-776-479-91	Sequence 91, Appl	180	17.6	0.3	35	9	US-09-895-814-815	Sequence 815, App
c 108	18	0.4	18	9	US-10-002-884A-6	Sequence 6, Appl	181	17.6	0.3	35	10	US-09-426-548-34	Sequence 34, Appl
c 109	18	0.4	18	9	US-10-300-247-51	Sequence 51, Appl	182	17.6	0.3	35	10	US-09-759-143-815	Sequence 815, App
c 110	18	0.4	18	10	US-09-824-468-59	Sequence 59, Appl	183	17.6	0.3	35	10	US-09-780-669-815	Sequence 815, App
c 111	18	0.4	18	10	US-09-824-468-104	Sequence 104, Appl	184	17.6	0.3	35	10	US-09-822-827-815	Sequence 815, App
c 112	18	0.4	18	10	US-09-965-116A-7	Sequence 7, Appl	c 185	17.6	0.3	38	9	US-09-780-533A-4212	Sequence 4212, Ap
c 113	18	0.4	18	10	US-09-965-116A-77	Sequence 77, Appl	c 186	17.6	0.3	39	9	US-10-080-980-24	Sequence 24, Appl
c 114	18	0.4	18	10	US-09-965-116A-98	Sequence 98, Appl	c 187	17.6	0.3	39	9	US-10-104-943-38	Sequence 38, Appl
c 115	18	0.4	18	10	US-09-965-116A-99	Sequence 99, Appl	c 188	17.6	0.3	39	9	US-10-104-943-82	Sequence 82, Appl
c 116	18	0.4	18	9	US-09-974-974-13	Sequence 13, Appl	c 189	17.6	0.3	39	9	US-10-104-943-84	Sequence 84, Appl
c 117	18	0.4	18	9	US-09-888-326-757	Sequence 757, Appl	c 190	17.6	0.3	39	9	US-10-104-943-88	Sequence 88, Appl
c 118	18	0.4	18	9	US-10-112-653-81	Sequence 81, Appl	c 191	17.6	0.3	39	9	US-10-104-943-90	Sequence 90, Appl
c 119	18	0.4	18	9	US-10-017-995-87	Sequence 87, Appl	192	17.6	0.3	40	9	US-10-222-952A-6	Sequence 6, Appl
c 120	18	0.4	18	9	US-09-982-262B-59	Sequence 59, Appl	c 193	17.6	0.3	40	10	US-09-790-417-215	Sequence 215, App
c 121	18	0.4	18	9	US-09-776-479-87	Sequence 87, Appl	c 194	17.6	0.3	40	10	US-09-245-802-4	Sequence 4, Appl
c 122	18	0.4	18	9	US-09-754-853A-601	Sequence 601, Appl	195	17.4	0.3	19	10	US-09-557-423-7	Sequence 7, Appl
c 123	18	0.4	18	9	US-10-066-151-92	Sequence 92, Appl	c 196	17.4	0.3	19	10	US-09-557-423-8	Sequence 8, Appl
c 124	18	0.4	18	9	US-09-817-587-12	Sequence 12, Appl	c 197	17.4	0.3	19	10	US-09-932-129-7	Sequence 7, Appl
c 125	18	0.4	18	9	US-10-183-695-1	Sequence 1, Appl	c 198	17.4	0.3	19	10	US-09-969-373-3086	Sequence 3086, Ap
c 126	18	0.4	18	9	US-10-085-906-126	Sequence 126, Appl	c 199	17.4	0.3	20	9	US-10-085-906-33	Sequence 33, Appl
c 127	18	0.4	18	9	US-10-134-021-12	Sequence 12, Appl	c 200	17.4	0.3	20	9	US-10-165-854-1	Sequence 1, Appl
c 128	18	0.4	18	9	US-09-810-796-16	Sequence 16, Appl	c 201	17.4	0.3	20	9	US-10-165-854-2	Sequence 2, Appl
c 129	18	0.4	18	9	US-09-828-034-5	Sequence 5, Appl	c 202	17.4	0.3	27	9	US-10-085-906-123	Sequence 123, App
c 130	18	0.4	18	9	US-10-208-357-4	Sequence 4, Appl	c 203	17.4	0.3	30	9	US-09-968-033C-9	Sequence 9, Appl
c 131	18	0.4	18	9	US-10-066-151-62	Sequence 62, Appl	c 204	17.4	0.3	30	9	US-09-984-842-2	Sequence 2, Appl
c 132	18	0.4	18	9	US-09-245-802-70	Sequence 70, Appl	c 205	17.4	0.3	30	10	US-09-932-129-9	Sequence 9, Appl
c 133	18	0.4	18	10	US-09-993-170-17	Sequence 17, Appl	c 206	17.4	0.3	31	9	US-10-194-138-1	Sequence 1, Appl
c 134	17.8	0.3	21	9	US-10-112-653-876	Sequence 876, Appl	c 207	17.4	0.3	31	10	US-09-801-274-450	Sequence 450, App
c 135	17.8	0.3	21	9	US-10-017-995-907	Sequence 907, Appl	c 208	17.4	0.3	31	10	US-09-801-274-1391	Sequence 1391, Ap
c 136	17.8	0.3	21	9	US-10-085-906-412	Sequence 412, Appl	c 209	17.4	0.3	33	9	US-10-021-330-1	Sequence 1, Appl
c 137	17.8	0.3	21	9	US-09-776-479-907	Sequence 907, Appl	c 210	17.4	0.3	33	9	US-09-852-416-23	Sequence 23, Appl
c 138	17.8	0.3	21	10	US-09-735-363A-19	Sequence 19, Appl	c 211	17.4	0.3	33	10	US-09-859-854-23	Sequence 23, Appl
c 139	17.8	0.3	21	10	US-09-735-363A-20	Sequence 20, Appl	c 212	17.4	0.3	34	9	US-10-114-893-256	Sequence 256, App
c 140	17.8	0.3	21	10	US-09-828-034-10	Sequence 10, Appl	c 213	17.4	0.3	34	9	US-10-124-880-54	Sequence 54, Appl
c 141	17.8	0.3	29	10	US-09-996-606-4	Sequence 4, Appl	c 214	17.4	0.3	34	10	US-09-765-272-380	Sequence 380, App
c 142	17.8	0.3	30	9	US-10-042-193A-1	Sequence 1, Appl	c 215	17.4	0.3	35	9	US-10-095-672A-20	Sequence 20, Appl
c 143	17.8	0.3	30	9	US-10-042-193A-2	Sequence 2, Appl	c 216	17.4	0.3	35	10	US-09-804-615-25	Sequence 25, Appl
c 144	17.8	0.3	30	9	US-10-217-914-4	Sequence 4, Appl	c 217	17.4	0.3	36	9	US-09-957-995A-24	Sequence 24, Appl
c 145	17.8	0.3	30	9	US-10-057-467-12	Sequence 12, Appl	c 218	17.4	0.3	36	9	US-09-961-404-14	Sequence 14, Appl
c 146	17.8	0.3	31	10	US-09-801-274-262	Sequence 262, Appl	c 219	17.4	0.3	36	10	US-09-828-034-4	Sequence 4, Appl
c 147	17.8	0.3	31	10	US-09-801-274-438	Sequence 438, Appl	c 220	17.4	0.3	36	10	US-09-932-129-10	Sequence 10, Appl
c 148	17.8	0.3	32	9	US-10-260-923-1	Sequence 1, Appl	c 221	17.4	0.3	36	10	US-09-870-203A-29	Sequence 29, Appl
c 149	17.8	0.3	32	10	US-09-456-038-1	Sequence 1, Appl	c 222	17.4	0.3	36	10	US-09-870-203A-30	Sequence 30, Appl
c 150	17.8	0.3	34	10	US-09-263-959-803	Sequence 803, Appl	c 223	17.4	0.3	37	10	US-10-085-906-225	Sequence 225, App
c 151	17.8	0.3	38	9	US-10-085-906-285	Sequence 285, Appl	c 224	17.4	0.3	37	9	US-10-194-550-15	Sequence 15, Appl
c 152	17.8	0.3	38	9	US-09-500-700-51	Sequence 51, Appl	c 225	17.4	0.3	37	10	US-09-758-317-1	Sequence 1, Appl
c 153	17.8	0.3	38	9	US-09-848-754A-5701	Sequence 5701, Ap	c 226	17.4	0.3	37	10	US-09-894-991-6	Sequence 6, Appl
c 154	17.8	0.3	39	9	US-09-934-060A-16	Sequence 16, Appl	c 227	17.4	0.3	38	9	US-10-208-357-2	Sequence 2, Appl
c 155	17.8	0.3	39	10	US-09-774-414-20	Sequence 20, Appl	c 228	17.4	0.3	38	9	US-09-780-164-1733	Sequence 1733, Ap
c 156	17.8	0.3	40	9	US-10-135-965-8	Sequence 8, Appl	c 229	17.4	0.3	38	10	US-09-774-414-27	Sequence 27, Appl
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c 165	17.6	0.3	24	9	US-09-974-546-71	Sequence 71, Appl	c 238	17.2	0.3	23	10	US-09-745-008-9	Sequence 9, Appl

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c 478 16.6 0.3 37 10 US-09-263-959-743 Sequence 743, Ap
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c 498 16.6 0.3 40 10 US-09-263-959-458 Sequence 458, Ap
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c 500 16.4 0.3 18 9 US-10-011-204-1 Sequence 1, Ap
c 501 16.4 0.3 18 9 US-10-011-204-2 Sequence 2, Ap

ALIGNMENTS

RESULT 1

US-10-085-906-27/c
; Sequence 27, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Ying, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; FILE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
; FILE REFERENCE: GNN-5343C2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens

RESULT 5

US-09-263-959-665/c
; Sequence 665, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTILIZE
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 665:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-665

Query Match 0.5%; Score 24.2; DB 10; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.3e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACAC 2338

Db 29 CACACACACACACACACACACACACAC 1

RESULT 6

US-09-920-342-9/c
; Sequence 9, Application US/09920342
; Patent No. US20020137709A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Lin, Shi-Lung
; APPLICANT: Chuong, Cheng-Ming
; APPLICANT: Widelitz, Randall B.
; TITLE OF INVENTION: GENE SILENCING USING MRNA-CDNA HYBRIDS
; FILE REFERENCE: 13761-7024
; CURRENT APPLICATION NUMBER: US/09/920,342
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 60/222,479
; PRIOR FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

US-09-920-342-9/c
; Sequence 9, Application US/09920342
; Patent No. US20020137709A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Lin, Shi-Lung
; APPLICANT: Chuong, Cheng-Ming
; APPLICANT: Widelitz, Randall B.
; TITLE OF INVENTION: GENE SILENCING USING MRNA-CDNA HYBRIDS
; FILE REFERENCE: 13761-7024
; CURRENT APPLICATION NUMBER: US/09/920,342
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 60/222,479
; PRIOR FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Anti-bcl2 primer
US-09-920-342-9

Query Match 0.5%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2725 CCATGCCCTCCCTGGCCTGAAGAAG 2748

Db 24 CCAATGCCCTCCCTGGCCTGAAGAAG 1

RESULT 7

US-09-920-342-11
; Sequence 11, Application US/09920342
; Patent No. US20020137709A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Lin, Shi-Lung
; APPLICANT: Chuong, Cheng-Ming
; APPLICANT: Widelitz, Randall B.
; TITLE OF INVENTION: GENE SILENCING USING MRNA-CDNA HYBRIDS
; FILE REFERENCE: 13761-7024
; CURRENT APPLICATION NUMBER: US/09/920,342
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 60/222,479
; PRIOR FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: bcl2 primer
US-09-920-342-11

Query Match 0.5%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1985 GGATGACTGAGTACCTGAACCGGC 2008

Db 1 GGATGACTGAGTACCTGAACCGGC 24

RESULT 8

US-09-735-363A-1/c
; Sequence 1, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-1

Query Match 0.5%; Score 23.8; DB 10; Length 27;
Best Local Similarity 92.6%; Pred. No. 1.6e+04;

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US-09-735-363A-5/C
; Sequence 5, Application US/09735363A
Patent No. US20010041681A1

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GENERAL INFORMATION:
APPLICANT: Filion, Mario
ATTORNEY: Philip, Nigel
TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
FILE REFERENCE: 02811-0181
CURRENT APPLICATION NUMBER: US/09/735,363A
CURRENT FILING DATE: 2000-12-12
PRIORITY FILING DATE: 1999-12-13
PRIORITY FILING DATE: 2000-12-12
PRIORITY FILING DATE: 1999-12-13
PRIORITY FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 27
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-5

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Query Match	0.5%;	Score 23.8;	DB 10;	Length 27;
Best Local Similarity	92.6%;	Pred. No. 1.6e+04;		
Matches 25; Conservative		0; Mismatches 2;	Indels 0;	Gaps 0;

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RESULT 10
US-09-735-363A-66/C
; Sequence 66 Patent Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically
; FILE REFERENCE: 02811-0181
; FILE REFREGISTRATION NUMBER: US/09735363A

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, CURRENT FILING DATE: 2000-12-12
, PRIOR APPLICATION NUMBER: 60/170,325
, PRIOR FILING DATE: 1999-12-13
, PRIOR APPLICATION NUMBER: 60/228,925
, PRIOR FILING DATE: 2000-08-29
, NUMBER OF SEQ ID NOS: 87
, SOFTWARE: PatentIn version 3.0
, SEQ ID NO 66
, LENGTH: 27
, TYPE: DNA
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Synthetic Oligonucleot
, US-09-735-363A-66

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Query Match	0.5%;	Score 23.8;	DB 10;	Length 27;
Best Local Similarity	92.6%;	Pred. No. 1.6e+04;		
Matches	25;	Conservative	0;	Mismatches 2;
			Indels	0;
			Gaps	0;

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US-09-263-959-770/c
US; sequence 770, Application US/09263959
; patent No. US20020150891A1

GENERAL INFORMATION:
APPLICANT: HOOD, Leroy E.
APPLICANT: ROSEN, Lee
APPLICANT: KOOP, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS: BERRY LLP

ADDRESSEE: Seed and Berry Ltd.
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092

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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE / DOCKET NUMBER: 920010.426C2

REFERENCE INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SSO ID NO: 770:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
CC 300-1770

Query Match	Score	DB	Length
Best Local Similarity	92.6%	Pred. No. 1.6e+04;	
Matches	25	Conservative	0; Mismatches 2; Indels

QY 2311 ACACACACAGACAGACACACACACA 2337
 ||||| ||| |||||
 rh 27 ACACACACACACACACACACACACA 1

REC'D. T 12

RES-012-12
US-95-0263-959-600/C
Sequence 600 Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC ANALYSIS OF
NUMBER OF SEQUENCES: 1279
NUMBER OF SEQUENCES: 1279

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed and Berry LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO

ULT 15
09-371-900-11/c
sequence 11, Application US/09371900
patent No. US20020137700A1
GENERAL INFORMATION:

us-09-375-514-19.rnpb

Sun Jun 1 14:55:56 2003

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 21
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide primers
US-09-931-732-21

Query Match 0.4%; Score 22; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1722 GGTGCCACCTGTGTCCACCTG 1743
Db 1 GGTGCCACCTGTGTCCACCTG 22

RESULT 17

US-09-925-674A-1
Sequence 1, Application US/09925674A
Patent No. US20020119943A1
GENERAL INFORMATION:
APPLICANT: AMRAD Operations Pty Ltd
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
FILE REFERENCE: 11686a
CURRENT APPLICATION NUMBER: US/09/925,674A
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/925,674
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: PN8965
PRIOR FILING DATE: 1996-03-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 33
TYPE: DNA
ORGANISM: Mouse
FEATURE:
NAME/KEY: modified_base
LOCATION: 16
OTHER INFORMATION: n is inosine
NAME/KEY: modified_base
LOCATION: 19
OTHER INFORMATION: n is inosine
NAME/KEY: modified_base
LOCATION: 22
OTHER INFORMATION: n is inosine
NAME/KEY: modified_base
LOCATION: 25
OTHER INFORMATION: n is inosine
US-09-925-674A-1

Query Match 0.4%; Score 21.4; DB 10; Length 33;
Best Local Similarity 74.1%; Pred. No. 7.6e+04; 4; Indels 0; Gaps 0;
Matches 20; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1884 GAACTGGGGAGGAGTGGCCTTCTT 1910
Db 7 GAACTGGGGAGGAGTGGCCTTCTT 33

RESULT 18

US-10-231-381-27
Sequence 27, Application US/10231381
Publication No. US20030096277A1
GENERAL INFORMATION:
APPLICANT: Chen, Xiangning
TITLE OF INVENTION: ALLELE SPECIFIC PCR FOR GENOTYPING
FILE REFERENCE: 02940201aa
CURRENT APPLICATION NUMBER: US/10/231,381
CURRENT FILING DATE: 2002-08-30

APPLICANT: FALB, DEAN A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/371,900
FILING DATE: 11-Aug-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995

ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-104
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic oligonucleotide"
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-371-900-11

Query Match 0.4%; Score 22.4; DB 10; Length 24;
Best Local Similarity 95.8%; Pred. No. 3.4e+04;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1875 GGACGGGTGAACCTGGGGAGGAT 1898
Db 24 GGATGGGTGAACCTGGGGAGGAT 1

RESULT 16

US-09-931-732-21
Sequence 21, Application US/09931732
Publication No. US20030045488A1
GENERAL INFORMATION:
APPLICANT: Brown, Bob D.
APPLICANT: Riley, Timothy A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES COMPRISING
UNIVERSAL AND/OR DEGENERATE BASES
FILE REFERENCE: OASBIO.001C1
CURRENT APPLICATION NUMBER: US/09/931,732
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: PCT/US00/09293
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US 60/128,377
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 30

; PRIOR APPLICATION NUMBER: 60/315,776
; CURRENT FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primer
US-10-231-381-27

Query Match 0.4%; Score 21.2; DB 9; Length 39;
Best Local Similarity 76.5%; Pred. No. 9.6e+04;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2300 ATATAACATCACACACACACACACACACACA 2333
Db 3 ATAACAATTTCACACACACCCACGCGTCAACCCACA 36

RESULT 19

US-09-925-674A-3/c
; Sequence 3, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: P88965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 14
; OTHER INFORMATION: n is inosine
; NAME/KEY: modified_base
; LOCATION: 17
; OTHER INFORMATION: n is inosine
; NAME/KEY: modified_base
; LOCATION: 20
; OTHER INFORMATION: n is inosine
US-09-925-674A-3

Query Match 0.4%; Score 21; DB 10; Length 31;
Best Local Similarity 80.8%; Pred. No. 9.2e+04;
Matches 21; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2020 TGGATCCAGGATAACGAGGCTGGGA 2045
Db 31 TGGATCCAGGANMANGNGGCTGGGA 6

RESULT 20

US-09-829-631A-3/c
; Sequence 3, Application US/09829631A
; Patent No. US20020091235A1
; GENERAL INFORMATION:
; APPLICANT: Sibley, David R.
; APPLICANT: Monsma, Frederick J.
; APPLICANT: Hamblin, Mark
; TITLE OF INVENTION: The ST-B17 Serotonin Receptor
; FILE REFERENCE: NIH047.1Cp1C1

; CURRENT APPLICATION NUMBER: US/09/829,631A
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 08/428,242
; PRIOR FILING DATE: 1995-09-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-829-631A-3

Query Match 0.4%; Score 21; DB 10; Length 33;
Best Local Similarity 82.8%; Pred. No. 9.6e+04;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4497 GGCTGTCTTCAGGCTCTCTGAAATGC 4525
Db 31 GGCTGGCTTCAAGCCCTTCCTGCTATGC 3

RESULT 21

US-09-764-891-10175/c
; Sequence 10175, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: EC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10175
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-10175

Query Match 0.4%; Score 21; DB 9; Length 30;
Best Local Similarity 73.0%; Pred. No. 1.1e+05;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1126 GCACCTGATTTTACTATTAGTTGTTTCTTT 1162
Db 38 GCACCTTTTCTTTTCTTTTCTTTTCTTTT 2

RESULT 22

US-10-112-653-1012/c
; Sequence 1012, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Daniel J.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1012
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide

us-09-375-514-19.rnpb

Sun Jun 1 14:55:56 2003

Db 24 CACACACACACACACACACACA 1

US-10-112-653-1012

Query Match 0.4%; Score 20.8; DB 9; Length 24;
Best Local Similarity 91.7%; Pred. No. 8.6e+04;
Matches 22; Conservative 0; Gaps 0;

QY 2310 CACACACACACACACACACACA 2333

Db 24 CACACACACACACACACACACA 1

RESULT 23

US-10-017-995-1068/c
; Sequence 1068, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1068
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-1068

Query Match 0.4%; Score 20.8; DB 9; Length 24;
Best Local Similarity 91.7%; Pred. No. 8.6e+04;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACA 2333

Db 24 CACACACACACACACACACACA 1

RESULT 24

US-09-776-479-1068/c
; Sequence 1068, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1068
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-1068

Query Match 0.4%; Score 20.8; DB 9; Length 24;
Best Local Similarity 91.7%; Pred. No. 8.6e+04;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACA 2333

Db 24 CACACACACACACACACACACA 1

Db 24 CACACACACACACACACACACA 1

RESULT 25

US-09-735-363A-21/c
; Sequence 21, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-21

Query Match 0.4%; Score 20.8; DB 10; Length 24;
Best Local Similarity 91.7%; Pred. No. 8.6e+04;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACA 2333

Db 24 CACACACACACACACACACACA 1

RESULT 26

US-09-735-363A-22/c
; Sequence 22, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-22

Query Match 0.4%; Score 20.8; DB 10; Length 24;
Best Local Similarity 91.7%; Pred. No. 8.6e+04;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2311 ACACACACACACACACACACAC 2334

Db 24 ACACACACACACACACACACAC 1

RESULT 27

US-10-085-906-189/c

; Sequence 189, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Ying, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; FILE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-085-906-189

Query Match 0.4%; Score 20.8; DB 9; Length 34;
Best Local Similarity 78.1%; Pred. No. 1.1e+05;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2312 CACACACAGACACACACACACACACAA 2343
DB 34 CAAACAAACACACACACACACACAAACAAAA 3

RESULT 28
US-09-931-732-22/c
; Sequence 22, Application US/09931732
; Publication No. US20030045488A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; APPLICANT: Riley, Timothy A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES COMPRISING
; FILE OF INVENTION: UNIVERSAL AND/OR DEGENERATE BASES
; FILE REFERENCE: OASBO 001C1
; CURRENT APPLICATION NUMBER: US/09/931,732
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: PCT/US00/09293
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/128,377
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primers
US-09-931-732-22

Query Match 0.4%; Score 20.4; DB 9; Length 22;
Best Local Similarity 95.5%; Pred. No. 1e+05;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2159 CCTATCTGAGCCCAAGTGAAG 2180
DB 22 CCTATCTGGGCCCAAGTGAAG 1

RESULT 29
US-09-949-305B-10/c
; Sequence 10, Application US/09949305B
; Publication No. US20030022318A1

; GENERAL INFORMATION:
; APPLICANT: Lin, Shi-Lung
; APPLICANT: Ying, Shao-Yao
; TITLE OF INVENTION: Method for Thermocycling Amplification of Nucleic Acid Sequences
; FILE REFERENCE: 266/014
; CURRENT APPLICATION NUMBER: US/09/949,305B
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/494,212
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense bcl-2 primer
US-09-949-305B-10

Query Match 0.4%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2729 GCCTCCCTGGCCTGAAGAAG 2748
DB 20 GCCTCCCTGGCCTGAAGAAG 1

RESULT 30
US-09-972-469-25
; Sequence 25, Application US/09972469
; Publication No. US20030073085A1
; GENERAL INFORMATION:
; APPLICANT: Lai, Fang
; APPLICANT: Zhou, Daixing
; TITLE OF INVENTION: AMPLIFYING EXPRESSED SEQUENCES FROM GENOMIC DNA OF HIGHER-ORDE
; FILE OF INVENTION: EUKARYOTIC ORGANISMS FOR DNA ARRAYS
; FILE REFERENCE: SP01-290
; CURRENT APPLICATION NUMBER: US/09/972,469
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-469-25

Query Match 0.4%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2783 TGGTGGGAGGAAAAGAGTTG 2802
DB 1 TGGTGGGAGGAAAAGAGTTG 20

RESULT 31
US-09-817-387-11/c
; Sequence 11, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
; APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof
; FILE REFERENCE: 101195-24
; CURRENT APPLICATION NUMBER: US/09/817,387
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: DE 197 20 151.2
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11

LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: oligonucleotides, linkages between positions 1
OTHER INFORMATION: to 20 are phosphorothioate, linkages between
OTHER INFORMATION: positions 20 to 28 are N3' to N5'
OTHER INFORMATION: phosphoramidates
OTHER INFORMATION: position 28 is modified by a 3'-aminodeoxyribosyl
OTHER INFORMATION: residue
US-09-817-387-11

Query Match 0.4%; Score 20; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1880 GGGTGAAGTGGGGGAGGATT 1899
Db 20 GGGTGAAGTGGGGGAGGATT 1

RESULT 32
US-09-801-274-1526/c
Sequence 1526, Application US/09801274
Patent No. US2002032319A1
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 60/206,129
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1526
LENGTH: 31
TYPE: DNA
ORGANISM: Homo sapiens
US-09-801-274-1526

Query Match 0.4%; Score 20; DB 10; Length 31;
Best Local Similarity 90.9%; Pred. No. 1.6e+05;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 73 CGTGGCGCGCGCGCGTGGC 94
Db 22 CGCTGCGCGCGCGCGTGGC 1

RESULT 33
US-09-864-785-1826
Sequence 1826, Application US/09864785
Patent No. US20020177568A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Stinchcomb, Dan
APPLICANT: Draper, Ken
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
TITLE OF INVENTION: Levels of NF-kappa B
FILE REFERENCE: 400/022 (MHH00-812-D)
CURRENT APPLICATION NUMBER: US/09/864,785
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 3929
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1826
LENGTH: 37

TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-1826

Query Match 0.4%; Score 20; DB 9; Length 37;
Best Local Similarity 69.4%; Pred. No. 1.9e+05;
Matches 25; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 162 CGGAGGTCGGGAGGCGACCGTAGTCGCGCCGCCG 197
Db 2 CGGAGGCGGAAAGCGGAGGAGGUCUCGCCGCGAG 37

RESULT 34
US-09-263-959-774
Sequence 774, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 774:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-774

Query Match 0.4%; Score 19.8; DB 10; Length 23;
Best Local Similarity 91.3%; Pred. No. 1.5e+05;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2313 ACACACAGACACACACACACA 2335
Db 1 ACACACACACATACACACACACA 23

RESULT 35
US-10-085-906-324/c
Sequence 324, Application US/10085906
Publication No. US20030054371A1
GENERAL INFORMATION:
APPLICANT: Ying, Vincent
APPLICANT: Wu, Paul
APPLICANT: Gray, Gary S.

; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 324
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-324

Query Match 0.4%; Score 19.8; DB 9; Length 32;
Best Local Similarity 77.4%; Pred. No. 1.9e+05;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2313 ACACACAGACACACACACACACACAA 2343
| | | | | | | | | | | | | | | | | | | |
Db 32 AAAAAACACACACACACACACACAAAAA 2

RESULT 36
US-09-923-327-60
; Sequence 60, Application US/09923327
; Publication No. US20030096236A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, Patricia D.
; TITLE OF INVENTION: Determining Common Functional Alleles in a Population and Uses Th
; FILE REFERENCE: 044921-5054-02
; CURRENT APPLICATION NUMBER: US/09/923,327
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/598,591
; PRIOR FILING DATE: 1996-02-12
; PRIOR APPLICATION NUMBER: US 08/798,691
; PRIOR FILING DATE: 1997-02-12
; PRIOR APPLICATION NUMBER: US 08/905,772
; PRIOR FILING DATE: 1997-08-04
; PRIOR APPLICATION NUMBER: US 09/084,471
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 09/129,134
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: US 09/524,794
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-923-327-60

Query Match 0.4%; Score 19.6; DB 9; Length 38;
Best Local Similarity 73.5%; Pred. No. 2.4e+05;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 3850 GAATCAGCCTTGAACATTTGATGTAATACTCTG 3883
| | | | | | | | | | | | | | | | | | | |
Db 4 GAAACAGCTATGACCATTTGTTAGTAGCTCTG 37

RESULT 37
US-10-231-381-26
; Sequence 26, Application US/10231381
; Publication No. US20030096277A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Xiangning

; TITLE OF INVENTION: ALLELE SPECIFIC PCR FOR GENOTYPING
; FILE REFERENCE: 02940201aa
; CURRENT APPLICATION NUMBER: US/10/231,381
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/315,776
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primer
US-10-231-381-26

Query Match 0.4%; Score 19.6; DB 9; Length 39;
Best Local Similarity 73.5%; Pred. No. 2.5e+05;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 2300 ATATAACATTCACACACAGACACACACACA 2333
| | | | | | | | | | | | | | | | | | | |
Db 3 ATAACAATTTCACACAGGACGCGTCAACCCACA 36

RESULT 38
US-09-828-034-12
; Sequence 12, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01185
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-12

Query Match 0.4%; Score 19.4; DB 10; Length 24;
Best Local Similarity 95.2%; Pred. No. 2e+05;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 18 CCGCTGCGCGCGCGCGCGCC 38
| | | | | | | | | | | | | | | | | | | |
Db 3 CCGCGCGCGCGCGCGCGCC 23

RESULT 39
US-09-966-781A-15/c
; Sequence 15, Application US/09966781A
; Publication No. US20030036184A1
; GENERAL INFORMATION:
; APPLICANT: SOULARD, PATRICIA
; TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR
; FILE REFERENCE: A0000281US
; CURRENT APPLICATION NUMBER: US/09/966,781A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP004026837
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1


```
Db 26 TCACAAATCCTAATAGATGCATAG 3
;
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 172
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphorothioate backbone
; US-09-888-326-172

Query Match 0.4%; Score 19; DB 9; Length 35;
Best Local Similarity 71.4%; Pred. No. 3.2e+05;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 CCGCGCCCTCGCGCGCGCTGCGCCGCCGCCGCCGCCGCC 38
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CCGCGCCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 35
| | | | | | | | | | | | | | | | | | | | | |

RESULT 47
US-10-112-653-744
; Sequence 744, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 744
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; US-10-112-653-744

Query Match 0.4%; Score 19; DB 9; Length 35;
Best Local Similarity 71.4%; Pred. No. 3.2e+05;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 CCGCGCCCTCGCGCGCGCTGCGCCGCCGCCGCCGCCGCC 38
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CCGCGCCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 35
| | | | | | | | | | | | | | | | | | | | | |

RESULT 48
US-10-017-995-771
; Sequence 771, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)

Db 26 TCACAAATCCTAATAGATGCATAG 3
;
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; TITLE OF INVENTION: AMPLIFICATION PRIMER PAIRS AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: OASBIO.002C1
; CURRENT APPLICATION NUMBER: US/09/932,129
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: PCT/US00/09230
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/128,378
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primers
; US-09-932-129-1

Query Match 0.4%; Score 19; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1725 GCCACCTGGTCCACCTG 1743
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GCCACCTGGTCCACCTG 19
| | | | | | | | | | | | | | | | | | | | | |

RESULT 45
US-09-992-665-377/C
; Sequence 377, Application US/0992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kala Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 377
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
; US-09-992-665-377

Query Match 0.4%; Score 19; DB 9; Length 30;
Best Local Similarity 81.5%; Pred. No. 2.9e+05;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4379 ATGACACGACGATTCATATCTATGGTG 4405
| | | | | | | | | | | | | | | | | | | | | |
Db 28 AGGTCCAGTAGATCCAAATCCATGGTG 2
| | | | | | | | | | | | | | | | | | | | | |

RESULT 46
US-09-888-326-172
; Sequence 172, Application US/09888326
; Publication No. US20030026801A1
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CURRENT APPLICATION NUMBER: US/10/017,995
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/255,534
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: fastseq for Windows Version 3.0
SEQ ID NO 771
LENGTH: 35
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-10-017-995-771

Query Match          0.4%;   Score 19;   DB 9;   Length 35;
Best Local Similarity 71.4%;   Pred. No. 3.2e+05;
Matches 25; Conservative 10; Mismatches 10; Gaps 0;

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RESULT 49
US-09-776-479-771
, Sequence 771, Application US/09776479
, Publication No. US20030087848A1
, GENERAL INFORMATION:
, APPLICANT: Bratzler, Robert L.
, APPLICANT: Petersen, Deanna M.
, APPLICANT: Fourn, Yves
, TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
, TITLE OF INVENTION: Treatment of Asthma and Allergy
, FILE REFERENCE: C1037/7013 (HCL/MAT)
, CURRENT APPLICATION NUMBER: US/09/776,479
, CURRENT FILING DATE: 2001-02-02
, PRIOR APPLICATION NUMBER: US 60/179,991
, PRIOR FILING DATE: 2000-02-03
, NUMBER OF SEQ ID NOS: 1093
, SOFTWARE: FastSeq for Windows Version 3.0
, SEQ ID NO 771

```

```

; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-771

Query Match          0.4%   Score 19;   DB 9;   Length 35;
Best local Similarity 71.4%   Pred. No. 3.2e+05;
Matches 25;   Conservative 0;   Mismatches 10;   Indels

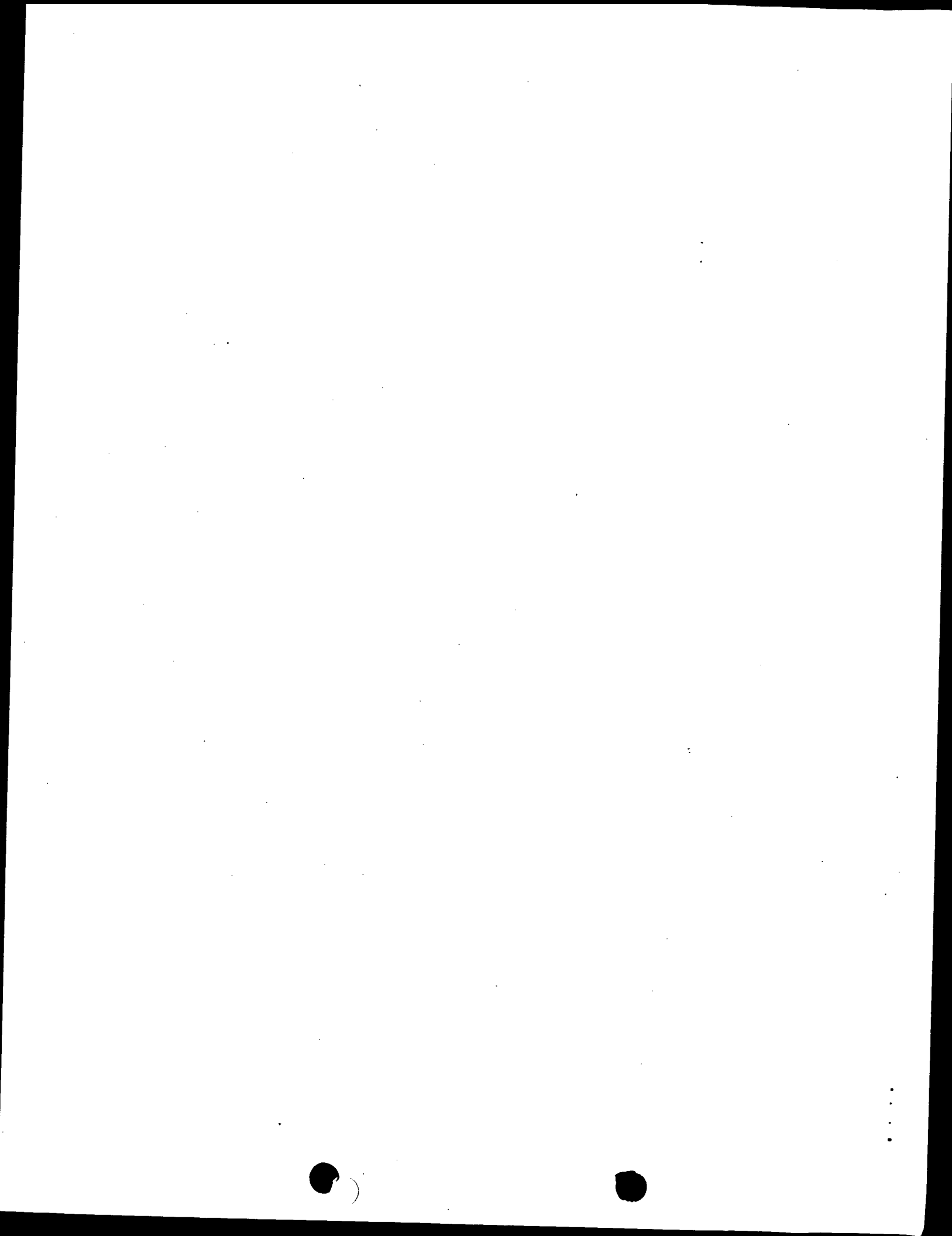
QY  4  CCGCGCCCTCCGGCGCGCTGCCCGCCGCCGCC 38
    ||| |||| ||| ||| ||| ||| ||| ||| |||
pb  1  CCGCGCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 35
    ||| |||| ||| ||| ||| ||| ||| ||| |||

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RESULT 50
US-09-932-129-4
; Sequence 4, Application US/09932129
; Patent No. US20020119533A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; TITLE OF INVENTION: AMPLIFICATION PRIMER PAIRS AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: OASBITO.002C1
; CURRENT APPLICATION NUMBER: US/09/932,129
; CURRENT FILING DATE: 2001-08-16
; PRIORITY APPLICATION NUMBER: PCT/US00/09230
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/128,378
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 12

```



101	21	0.4	35	2	US-08-619-542B-9	Sequence 9, Appli	174	19.4	0.4	35	2	US-08-619-542B-12	Sequence 12, Appl
102	21	0.4	35	2	US-08-619-542B-10	Sequence 10, Appli	175	19.4	0.4	35	2	US-08-619-542B-13	Sequence 13, Appl
c 103	20.8	0.4	24	1	US-08-182-619-3	Sequence 3, Appli	c 176	19.4	0.4	38	4	US-08-470-369-24	Sequence 24, Appl
c 104	20.8	0.4	24	1	US-08-222-177A-445	Sequence 445, App	c 177	19.4	0.4	38	6	US-08-470-369-24	Sequence 24, Appl
c 105	20.8	0.4	24	1	US-08-330-535A-3	Sequence 3, Appli	c 178	19.4	0.4	39	1	US-07-971-160-40	Sequence 40, Appl
c 106	20.8	0.4	24	1	US-08-838-844-3	Sequence 3, Appli	c 179	19.4	0.4	39	1	US-08-068-747-9	Sequence 9, Appli
c 107	20.8	0.4	24	1	US-08-849-021-2	Sequence 1, Appli	c 180	19.4	0.4	39	1	US-08-336-241-40	Sequence 40, Appl
c 108	20.8	0.4	24	1	US-08-849-021-2	Sequence 2, Appli	c 181	19.4	0.4	39	1	US-08-465-273-40	Sequence 40, Appl
c 109	20.8	0.4	24	1	US-08-677-045-10	Sequence 10, Appli	c 182	19.4	0.4	39	2	US-08-113-024-40	Sequence 40, Appl
c 110	20.6	0.4	27	1	US-08-410-804-13	Sequence 13, Appli	c 183	19.4	0.4	39	2	US-08-417-226-40	Sequence 40, Appl
c 111	20.6	0.4	27	1	US-08-607-269-8	Sequence 8, Appli	c 184	19.4	0.4	39	2	US-08-417-226-40	Sequence 40, Appl
c 112	20.6	0.4	27	1	US-08-259-514-13	Sequence 13, Appli	c 185	19.4	0.4	39	4	US-08-196-131-40	Sequence 40, Appl
c 113	20.6	0.4	27	1	US-08-858-311-13	Sequence 13, Appli	c 186	19.4	0.4	39	4	US-08-643-732-40	Sequence 40, Appl
c 114	20.6	0.4	27	1	PCT-US95-04600-8	Sequence 8, Appli	c 187	19.4	0.4	40	4	US-09-306-290-28	Sequence 28, Appl
c 115	20.6	0.4	28	2	US-08-762-106-11	Sequence 11, Appli	c 188	19.4	0.4	40	4	US-09-569-572C-5	Sequence 5, Appli
c 116	20.6	0.4	28	2	US-08-320-774-11	Sequence 11, Appli	c 189	19.4	0.4	40	4	US-09-569-572C-5	Sequence 5, Appli
c 117	20.4	0.4	37	1	US-08-360-125-1	Sequence 1, Appli	c 190	19.2	0.4	24	1	US-08-014-943A-6	Sequence 6, Appli
c 118	20.4	0.4	37	2	US-08-450-578-1	Sequence 1, Appli	c 191	19.2	0.4	24	1	US-08-486-421-43	Sequence 43, Appl
c 119	20.4	0.4	37	2	US-09-017-828-1	Sequence 1, Appli	c 192	19.2	0.4	24	1	US-08-470-911-43	Sequence 43, Appl
c 120	20.4	0.4	37	2	US-09-014-880-1	Sequence 1, Appli	c 193	19.2	0.4	24	2	US-08-486-809-43	Sequence 43, Appl
c 121	20.4	0.4	37	4	US-08-450-363-1	Sequence 1, Appli	c 194	19.2	0.4	24	3	US-08-624-290B-9	Sequence 9, Appli
c 122	20.4	0.4	38	4	US-09-459-884-12	Sequence 12, Appli	c 195	19.2	0.4	28	3	US-08-993-008A-1	Sequence 1, Appli
c 123	20.2	0.4	26	5	PCT-US92-10792-44	Sequence 44, Appli	c 196	19.2	0.4	32	4	US-09-813-781-79	Sequence 79, Appl
c 124	20.2	0.4	28	3	US-08-915-609-2	Sequence 2, Appli	c 197	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
c 125	20.2	0.4	33	1	US-08-068-747-7	Sequence 7, Appli	c 198	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
c 126	20.2	0.4	33	6	5478746-1	Patent No. 5478746	c 199	19.2	0.4	35	1	US-08-465-811A-13	Sequence 13, Appl
c 127	20	0.4	20	1	US-08-217-082A-1	Sequence 1, Appli	c 200	19.2	0.4	35	1	US-08-465-811A-13	Sequence 13, Appl
c 128	20	0.4	20	1	US-08-217-082A-7	Sequence 7, Appli	c 201	19.2	0.4	35	2	US-08-619-542B-13	Sequence 13, Appl
c 129	20	0.4	20	1	US-08-405-702A-13	Sequence 13, Appli	c 202	19.2	0.4	35	2	US-08-619-542B-13	Sequence 13, Appl
c 130	20	0.4	20	1	US-08-405-702A-14	Sequence 14, Appli	c 203	19.2	0.4	36	1	US-08-444-005-4	Sequence 4, Appli
c 131	20	0.4	20	2	US-08-465-485A-14	Sequence 14, Appli	c 204	19.2	0.4	40	1	US-08-390-878-9	Sequence 9, Appli
c 132	20	0.4	20	2	US-08-465-485A-7	Sequence 7, Appli	c 205	19.2	0.4	40	1	US-09-306-290-20	Sequence 20, Appl
c 133	20	0.4	20	2	US-08-465-485A-26	Sequence 26, Appli	c 206	19	0.4	40	1	US-07-936-421-1	Sequence 1, Appli
c 134	20	0.4	20	2	US-08-465-485A-28	Sequence 28, Appli	c 207	19	0.4	40	1	US-07-936-421-11	Sequence 11, Appli
c 135	20	0.4	20	3	US-09-080-285-1	Sequence 1, Appli	c 208	19	0.4	40	1	US-07-936-421-12	Sequence 12, Appli
c 136	20	0.4	20	3	US-09-080-285-7	Sequence 7, Appli	c 209	19	0.4	40	1	US-07-936-421-14	Sequence 14, Appli
c 137	20	0.4	20	3	US-09-080-285-26	Sequence 26, Appli	c 210	19	0.4	32	3	US-08-694-869-6	Sequence 6, Appli
c 138	20	0.4	20	3	US-09-080-285-28	Sequence 28, Appli	c 211	19	0.4	32	3	US-09-349-546-6	Sequence 6, Appli
c 139	20	0.4	20	4	US-09-445-486-1	Sequence 1, Appli	c 212	19	0.4	38	1	US-08-219-012-91	Sequence 91, Appli
c 140	20	0.4	20	4	US-09-445-486-2	Sequence 2, Appli	c 213	19	0.4	38	1	US-08-276-271-2	Sequence 2, Appli
c 141	20	0.4	20	4	US-09-445-486-3	Sequence 3, Appli	c 214	19	0.4	38	3	US-08-434-463-6	Sequence 6, Appli
c 142	20	0.4	20	4	US-09-445-486-4	Sequence 4, Appli	c 215	19	0.4	38	4	US-08-687-421-279	Sequence 279, App
c 143	20	0.4	20	4	US-09-378-718-1	Sequence 1, Appli	c 216	19	0.4	38	4	US-09-325-554-8	Sequence 8, Appli
c 144	20	0.4	20	4	US-09-378-718-2	Sequence 2, Appli	c 217	19	0.4	38	4	US-09-569-572C-6	Sequence 6, Appli
c 145	20	0.4	20	4	US-09-724-426-1	Sequence 1, Appli	c 218	19	0.4	38	4	PCT-US95-09237-2	Sequence 2, Appli
c 146	20	0.4	20	4	US-09-724-426-7	Sequence 7, Appli	c 219	19	0.4	38	5	US-08-222-177A-331	Sequence 331, App
c 147	20	0.4	20	4	US-09-724-426-26	Sequence 26, Appli	c 220	19	0.4	39	1	US-08-479-783A-90	Sequence 90, Appl
c 148	20	0.4	20	4	US-09-724-426-28	Sequence 28, Appli	c 221	19	0.4	39	1	US-08-479-783A-90	Sequence 90, Appl
c 149	20	0.4	20	4	US-09-301-836-1	Sequence 1, Appli	c 222	19	0.4	39	1	US-08-618-693-88	Sequence 88, Appl
c 150	20	0.4	20	4	US-09-301-836-2	Sequence 2, Appli	c 223	19	0.4	39	2	US-08-973-124-177	Sequence 177, App
c 151	20	0.4	20	4	US-08-798-897-8	Sequence 8, Appli	c 224	19	0.4	39	4	US-08-991-743C-88	Sequence 88, Appl
c 152	20	0.4	20	4	US-08-798-897-8	Sequence 8, Appli	c 225	19	0.4	39	4	US-08-590-563-31	Sequence 31, Appli
c 153	20	0.4	20	4	US-08-390-858B-12	Sequence 12, Appli	c 226	19	0.4	39	4	US-09-569-572C-7	Sequence 7, Appli
c 154	20	0.4	20	4	US-09-249-585A-11	Sequence 11, Appli	c 227	19	0.4	39	5	PCT-US96-08014-177	Sequence 177, App
c 155	19.8	0.4	33	4	US-08-222-177A-454	Sequence 454, App	c 228	19	0.4	40	2	US-08-857-946-90	Sequence 90, Appl
c 156	19.8	0.4	23	1	US-08-993-008A-2	Sequence 2, Appli	c 229	19	0.4	40	3	US-08-970-740-90	Sequence 90, Appl
c 157	19.8	0.4	23	1	US-08-993-008A-3	Sequence 3, Appli	c 230	19	0.4	40	4	US-09-306-290-31	Sequence 31, Appl
c 158	19.8	0.4	23	1	US-08-993-008A-4	Sequence 4, Appli	c 231	19	0.4	40	4	US-09-306-290-35	Sequence 35, Appl
c 159	19.8	0.4	23	1	US-08-993-008A-5	Sequence 5, Appli	c 232	19	0.4	40	4	US-08-222-177A-125	Sequence 125, App
c 160	19.6	0.4	39	4	US-09-425-638A-17	Sequence 17, Appli	c 233	19	0.4	22	1	US-08-014-943A-9	Sequence 9, Appli
c 161	19.6	0.4	39	4	US-09-543-004-17	Sequence 4, Appli	c 234	18.8	0.4	24	1	US-08-486-421-48	Sequence 48, Appl
c 162	19.6	0.4	40	1	US-07-949-488A-6	Sequence 6, Appli	c 235	18.8	0.4	24	1	US-08-470-911-48	Sequence 48, Appl
c 163	19.4	0.4	21	1	US-08-182-619-4	Sequence 4, Appli	c 236	18.8	0.4	24	2	US-08-486-809-48	Sequence 48, Appl
c 164	19.4	0.4	21	1	US-08-330-535A-4	Sequence 4, Appli	c 237	18.8	0.4	24	2	US-08-374-144-3	Sequence 3, Appli
c 165	19.4	0.4	21	2	US-08-838-844-4	Sequence 4, Appli	c 238	18.8	0.4	25	1	US-08-775-164-3	Sequence 3, Appli
c 166	19.4	0.4	32	1	US-08-126-594-8	Sequence 8, Appli	c 239	18.8	0.4	25	2	US-08-775-609-3	Sequence 3, Appli
c 167	19.4	0.4	32	1	US-08-465-811A-8	Sequence 8, Appli	c 240	18.8	0.4	25	2	PCT-US93-06828-3	Sequence 3, Appli
c 168	19.4	0.4	32	2	US-08-619-542B-8	Sequence 8, Appli	c 241	18.8	0.4	25	5	US-08-915-609-1	Sequence 1, Appli
c 169	19.4	0.4	35	1	US-08-126-594-12	Sequence 12, Appli	c 242	18.8	0.4	27	3	US-08-482-842B-7	Sequence 7, Appli
c 170	19.4	0.4	35	1	US-08-126-594-15	Sequence 15, Appli	c 243	18.8	0.4	35	2	US-09-174-465D-16	Sequence 16, Appl
c 171	19.4	0.4	35	1	US-08-465-811A-12	Sequence 12, Appli	c 244	18.8	0.4	35	2		
c 172	19.4	0.4	35	1	US-08-465-811A-15	Sequence 15, Appli	c 245	18.8	0.4	35	2		
c 173	19.4	0.4	35	1	US-08-465-811A-15	Sequence 15, Appli	c 246	18.8	0.4	35	4		

247	18.8	0.4	35	4	US-09-599-564A-16	Sequence 16, Appl	320	18.2	0.4	39	4	US-09-260-952A-8	Sequence 8, Appl
c 248	18.8	0.4	38	1	US-08-373-124A-635	Sequence 635, App	321	18.2	0.4	39	4	US-09-253-341-8	Sequence 8, Appl
c 249	18.8	0.4	38	1	US-08-435-628-635	Sequence 635, App	322	18.2	0.4	39	4	US-09-253-331A-8	Sequence 8, Appl
250	18.8	0.4	40	1	US-08-484-686B-35	Sequence 35, Appl	323	18.2	0.4	39	4	US-09-337-635-20	Sequence 20, Appl
251	18.8	0.4	40	1	US-08-463-160B-35	Sequence 35, Appl	324	18.2	0.4	39	4	US-09-261-040-8	Sequence 8, Appl
c 252	18.6	0.4	28	3	US-08-863-813A-38	Sequence 38, Appl	325	18.2	0.4	39	4	US-09-097-319A-21	Sequence 21, Appl
c 253	18.6	0.4	28	4	US-08-676-318A-38	Sequence 38, Appl	326	18.2	0.4	39	4	US-09-337-280-20	Sequence 20, Appl
c 254	18.6	0.4	30	1	US-08-467-126-1	Sequence 1, Appl	c 327	18.2	0.4	40	1	US-08-231-342-12	Sequence 12, Appl
255	18.6	0.4	30	2	US-08-629-001A-75	Sequence 75, Appl	328	18.2	0.4	40	2	US-08-117-981-11	Sequence 11, Appl
c 256	18.6	0.4	30	2	US-08-476-712-3	Sequence 3, Appl	329	18.2	0.4	40	2	US-08-477-081-11	Sequence 11, Appl
c 257	18.6	0.4	30	4	US-08-642-274D-154	Sequence 154, App	330	18.2	0.4	40	4	US-09-306-290-2	Sequence 2, Appl
c 258	18.6	0.4	34	1	US-09-411-291-3	Sequence 3, Appl	331	18.2	0.4	40	4	US-09-453-195A-10	Sequence 10, Appl
c 259	18.6	0.4	34	1	US-08-434-503-29	Sequence 29, Appl	c 332	18.2	0.4	40	4	US-09-538-709-1236	Sequence 1236, App
c 260	18.6	0.4	35	1	US-08-126-594-20	Sequence 20, Appl	333	18.2	0.4	40	5	PCT-US93-02142-11	Sequence 11, Appl
c 261	18.6	0.4	35	1	US-08-465-811A-20	Sequence 20, Appl	c 334	18	0.4	18	1	US-08-217-082A-17	Sequence 17, Appl
c 262	18.6	0.4	35	2	US-08-619-542B-20	Sequence 20, Appl	c 335	18	0.4	18	2	US-08-465-485A-17	Sequence 17, Appl
c 263	18.6	0.4	40	1	US-08-510-032A-2	Sequence 2, Appl	c 336	18	0.4	18	2	US-08-465-485A-24	Sequence 24, Appl
c 264	18.6	0.4	40	2	US-08-723-306-17	Sequence 17, Appl	337	18	0.4	18	3	US-08-894-784-14	Sequence 14, Appl
c 265	18.6	0.4	40	3	US-08-688-514-2	Sequence 2, Appl	c 338	18	0.4	18	3	US-08-894-784-34	Sequence 34, Appl
c 266	18.6	0.4	40	4	US-09-506-729-5	Sequence 5, Appl	c 339	18	0.4	18	3	US-08-894-784-35	Sequence 35, Appl
c 267	18.6	0.4	40	5	PCT-US96-10041-17	Sequence 17, Appl	c 340	18	0.4	18	3	US-09-080-285-17	Sequence 17, Appl
c 268	18.6	0.4	20	4	US-09-109-663-72	Sequence 72, Appl	c 341	18	0.4	18	3	US-09-080-285-24	Sequence 24, Appl
c 269	18.4	0.4	31	1	US-08-467-126-4	Sequence 4, Appl	c 342	18	0.4	18	3	US-09-249-730-218	Sequence 218, App
270	18.4	0.4	31	3	US-08-738-381-24	Sequence 24, Appl	c 343	18	0.4	18	3	US-09-118-220-1	Sequence 1, Appl
c 271	18.4	0.4	35	1	US-07-931-473B-206	Sequence 206, App	c 344	18	0.4	18	4	US-08-738-652-55	Sequence 55, Appl
c 272	18.4	0.4	35	1	US-07-714-131C-206	Sequence 206, App	c 345	18	0.4	18	4	US-09-030-701-27	Sequence 27, Appl
c 273	18.4	0.4	35	1	US-08-412-110-206	Sequence 206, App	c 346	18	0.4	18	4	US-09-286-098-59	Sequence 59, Appl
c 274	18.4	0.4	35	2	US-08-409-442A-206	Sequence 206, App	c 347	18	0.4	18	4	US-09-286-098-59	Sequence 59, Appl
c 275	18.4	0.4	35	2	US-08-469-609A-206	Sequence 206, App	c 348	18	0.4	18	4	US-08-960-098-104	Sequence 104, App
c 276	18.4	0.4	35	3	US-09-143-190-206	Sequence 206, App	c 349	18	0.4	18	4	US-09-078-954-14	Sequence 14, Appl
c 277	18.4	0.4	36	1	US-09-502-344-206	Sequence 206, App	c 350	18	0.4	18	4	US-09-325-193A-51	Sequence 51, Appl
c 278	18.4	0.4	36	1	US-08-093-453B-12	Sequence 12, Appl	c 351	18	0.4	18	4	US-09-724-426-17	Sequence 17, Appl
279	18.4	0.4	36	2	US-08-459-041A-9	Sequence 9, Appl	c 352	18	0.4	18	4	US-09-724-426-24	Sequence 24, Appl
c 280	18.4	0.4	36	2	US-08-596-387B-113	Sequence 113, App	c 353	18	0.4	18	4	US-09-191-170-53	Sequence 53, Appl
c 281	18.4	0.4	36	2	US-08-863-639A-31	Sequence 31, Appl	354	18	0.4	20	1	US-08-063-167A-59	Sequence 59, Appl
c 282	18.4	0.4	36	4	US-09-067-615-113	Sequence 113, App	355	18	0.4	20	2	US-08-007-997A-59	Sequence 59, Appl
c 283	18.4	0.4	36	4	US-09-462-569B-4	Sequence 4, Appl	356	18	0.4	20	2	US-08-440-740A-59	Sequence 59, Appl
c 284	18.4	0.4	36	5	PCT-US95-09816A-113	Sequence 113, App	357	18	0.4	20	2	US-08-344-155C-59	Sequence 59, Appl
c 285	18.4	0.4	37	1	US-08-113-646A-4	Sequence 4, Appl	358	18	0.4	20	3	US-08-982-845B-59	Sequence 59, Appl
c 286	18.4	0.4	40	2	US-08-771-624B-1	Sequence 1, Appl	359	18	0.4	20	3	US-08-991-525B-59	Sequence 59, Appl
c 287	18.4	0.4	40	2	US-08-440-209-4	Sequence 4, Appl	360	18	0.4	20	3	US-09-085-759-59	Sequence 59, Appl
c 288	18.4	0.4	40	3	US-08-439-996-4	Sequence 4, Appl	361	18	0.4	20	3	US-09-128-496-59	Sequence 59, Appl
c 289	18.4	0.4	40	4	US-09-306-290-36	Sequence 36, Appl	362	18	0.4	20	4	US-09-009-490A-59	Sequence 59, Appl
c 290	18.4	0.4	40	4	US-09-732-067-7	Sequence 7, Appl	c 363	18	0.4	20	4	US-09-082-649B-60	Sequence 60, Appl
c 291	18.2	0.4	27	5	PCT-US92-10793-45	Sequence 45, Appl	364	18	0.4	20	5	PCT-US93-08101-59	Sequence 59, Appl
c 292	18.2	0.4	31	1	US-09-009-913-103	Sequence 103, App	c 365	18	0.4	25	1	US-08-182-619-13	Sequence 13, Appl
c 293	18.2	0.4	31	1	US-08-145-704-9	Sequence 9, Appl	c 366	18	0.4	25	1	US-08-390-858B-13	Sequence 13, Appl
c 294	18.2	0.4	31	3	US-08-987-574-9	Sequence 9, Appl	c 367	18	0.4	25	1	US-08-330-535A-13	Sequence 13, Appl
c 295	18.2	0.4	31	4	US-08-535-168-9	Sequence 9, Appl	c 368	18	0.4	25	2	US-08-838-844-13	Sequence 13, Appl
c 296	18.2	0.4	31	4	US-09-017-974-9	Sequence 9, Appl	c 369	18	0.4	26	1	US-08-487-141B-42	Sequence 42, Appl
c 297	18.2	0.4	31	4	US-08-682-255A-9	Sequence 9, Appl	c 370	18	0.4	26	2	US-08-937-561-42	Sequence 42, Appl
c 298	18.2	0.4	31	4	US-09-429-130-9	Sequence 9, Appl	c 371	18	0.4	26	5	PCT-US96-09388-42	Sequence 42, Appl
c 299	18.2	0.4	31	5	PCT-US96-11786-9	Sequence 9, Appl	372	18	0.4	30	1	US-08-504-511A-6	Sequence 6, Appl
c 300	18.2	0.4	32	5	PCT-US96-08142-4	Sequence 4, Appl	373	18	0.4	30	1	US-08-467-126-6	Sequence 6, Appl
c 301	18.2	0.4	33	3	US-09-061-026-26	Sequence 26, App	374	18	0.4	30	2	US-08-629-001A-44	Sequence 44, Appl
c 302	18.2	0.4	33	3	US-09-466-138-26	Sequence 26, Appl	375	18	0.4	30	2	US-08-476-712-5	Sequence 5, Appl
c 303	18.2	0.4	34	2	US-08-435-149-24	Sequence 24, Appl	376	18	0.4	30	4	US-08-642-274D-123	Sequence 123, App
c 304	18.2	0.4	36	2	US-08-596-387B-112	Sequence 112, App	377	18	0.4	31	4	US-09-411-291-5	Sequence 5, Appl
c 305	18.2	0.4	36	4	US-09-067-615-112	Sequence 112, App	378	18	0.4	31	4	US-09-268-505B-13	Sequence 13, Appl
c 306	18.2	0.4	36	5	PCT-US95-09816A-112	Sequence 112, App	c 379	18	0.4	35	1	US-07-844-297-2	Sequence 2, Appl
c 307	18.2	0.4	38	1	US-08-399-696-6	Sequence 6, Appl	380	18	0.4	35	1	US-08-435-350-118	Sequence 118, App
c 308	18.2	0.4	38	2	US-08-467-822-16	Sequence 16, Appl	381	18	0.4	37	1	US-08-435-350-3	Sequence 3, Appl
c 309	18.2	0.4	38	4	US-08-432-697-16	Sequence 16, Appl	c 382	18	0.4	37	1	US-07-915-245-1	Sequence 1, Appl
c 310	18.2	0.4	38	4	US-08-466-248-16	Sequence 16, Appl	383	18	0.4	38	1	US-07-906-871-16	Sequence 16, Appl
c 311	18.2	0.4	38	4	US-09-410-903-73	Sequence 73, Appl	c 384	18	0.4	38	1	US-08-145-704-2	Sequence 2, Appl
c 312	18.2	0.4	39	2	US-08-980-071-20	Sequence 20, Appl	c 385	18	0.4	38	1	US-08-145-704-4	Sequence 4, Appl
c 313	18.2	0.4	39	2	US-08-757-536-20	Sequence 20, Appl	c 386	18	0.4	38	3	US-08-987-574-2	Sequence 2, Appl
c 314	18.2	0.4	39	3	US-08-754-490-8	Sequence 8, Appl	c 387	18	0.4	38	3	US-08-987-574-4	Sequence 4, Appl
c 315	18.2	0.4	39	3	US-09-314-093-20	Sequence 20, Appl	c 388	18	0.4	38	4	US-08-535-168-2	Sequence 2, Appl
c 316	18.2	0.4	39	3	US-08-922-505A-8	Sequence 8, Appl	c 389	18	0.4	38	4	US-08-535-168-4	Sequence 4, Appl
c 317	18.2	0.4	39	3	US-09-250-848-20	Sequence 20, Appl	c 390	18	0.4	38	4	US-09-017-974-2	Sequence 2, Appl
c 318	18.2	0.4	39	4	US-09-251-885-20	Sequence 20, Appl	c 391	18	0.4	38	4	US-09-017-974-4	Sequence 4, Appl
c 319	18.2	0.4	39	4	US-09-306-290-40	Sequence 40, Appl	c 392	18	0.4	38	4	US-08-682-255A-2	Sequence 2, Appl

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486 17.6 0.3 33 4 US-08-623-428B-8
487 17.6 0.3 33 5 PCT-US93-08329-15
488 17.6 0.3 33 5 PCT-US94-05378-4
489 17.6 0.3 34 2 US-08-612-840A-9
490 17.6 0.3 34 2 US-08-933-821-11
491 17.6 0.3 34 3 US-08-960-507-11
492 17.6 0.3 34 4 US-09-136-828-11
493 17.6 0.3 34 4 US-09-332-928A-11
494 17.6 0.3 34 4 US-09-136-801-11
495 17.6 0.3 34 4 US-09-332-929-11
496 17.6 0.3 35 1 US-08-126-594-11
497 17.6 0.3 35 1 US-08-465-811A-11
498 17.6 0.3 35 2 US-08-619-542B-11
499 17.6 0.3 35 4 US-09-159-106-8
500 17.6 0.3 35 4 US-09-605-785-815

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Sequence 11, Appli
Sequence 8, Appli
Sequence 815, App

ALIGNMENTS

RESULT 1
US-07-936-421-2
Sequence 2, Application US/07936421
Patent No. 5750390
GENERAL INFORMATION:
APPLICANT: James D. Thompson
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: METHOD AND REAGENT FOR
TREATMENT OF DISEASES CAUSED
BY EXPRESSION OF THE BCL-2
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/936,421
FILING DATE: 19920826
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
none

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 197/243
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 37
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-936-421-2

Query Match 0.7%; Score 37; DB 1; Length 37;
Best Local Similarity 70.3%; Pred. No. 2.6;
Matches 26; Conservative 11; Mismatches 0; Indels 0; Gaps 0;
QY 1415 GCGAGAGGTGCGTGGCCCGCGTGTTCCTCT 1451
DB 1 GCGAGAGGCGCGUUGCCCGCGUUCUUCU 37

RESULT 2
US-07-936-421-15
; Sequence 15, Application US/07936421
; Patent No. 5750390
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: TREATMENT OF DISEASES CAUSED
; TITLE OF INVENTION: BY EXPRESSION OF THE BCL-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/936,421
; FILING DATE: 19920826
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/243
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-936-421-15

Query Match 0.7%; Score 36; DB 1; Length 36;
Best Local Similarity 86.1%; Pred. No. 4.5;
Matches 31; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1997 ACCTGAACCGGCACCTGCACACCTGGATCCAGGATA 2032
DB 1 ACCUGAACCGGCACCGCAGCACCUGGAGCAUUA 36

RESULT 3
US-08-217-082A-2
; Sequence 2, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 224 Airport Parkway
; CITY: San Jose
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 95110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,082A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-08-217-082A-2
Query Match 0.7%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1442 CTTTCTCTCTGGAGGATGGCGCAGCTGGGAGA 1476
DB 1 CTTTCTCTCTGGAGGATGGCGCAGCTGGGAGA 35

RESULT 4
US-07-936-421-20
; Sequence 20, Application US/07936421
; Patent No. 5750390
; GENERAL INFORMATION:

;; FILING DATE: 21-FEB-1992
;; PRIOR APPLICATION DATA: US 07/288,692
;; APPLICATION NUMBER: 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;; FILING DATE: 22-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fortney, Andrew D.
;; REGISTRATION NUMBER: 34,600
;; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (408) 436-2070
;; TELEFAX: (408) 436-2075
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 35 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; ANTI-SENSE: NO
US-09-080-285-2

Query Match 0.7%; Score 35; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1442 CTTTTCCTCTGGGAAGGATGCGCAGCTGGGAGA 1476
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Db 1 CTTTTCCTCTGGGAAGGATGCGCAGCTGGGAGA 35

RESULT 7
US-09-724-426-2
;; Sequence 2, Application US/09724426
;; Patent No. 6414134
;; GENERAL INFORMATION:
;; APPLICANT: Reed, John
;; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
;; FILE REFERENCE: 10412-024
;; CURRENT APPLICATION NUMBER: US/09/724,426
;; CURRENT FILING DATE: 2000-11-28
;; NUMBER OF SEQ ID NOS: 29
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 2
;; LENGTH: 35
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-724-426-2

Query Match 0.7%; Score 35; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1442 CTTTTCCTCTGGGAAGGATGCGCAGCTGGGAGA 1476
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Db 1 CTTTTCCTCTGGGAAGGATGCGCAGCTGGGAGA 35

RESULT 8
US-07-936-421-16
;; Sequence 16, Application US/07936421
;; Patent No. 5750390
;; GENERAL INFORMATION:
;; APPLICANT: James D. Thompson
;; APPLICANT: Kenneth G. Draper
;; TITLE OF INVENTION: METHOD AND REAGENT FOR
;; TREATMENT OF DISEASES CAUSED
;; BY EXPRESSION OF THE BCL-2
;; TITLE OF INVENTION: GENE
;; NUMBER OF SEQUENCES: 22
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 611 West Sixth Street
;; CITY: Los Angeles

;; STATE: California
;; COUNTRY: USA
;; ZIP: 90017
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
;; SOFTWARE: WordPerfect (Version 5.1)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/936,421
;; FILING DATE: 19920826
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; PRIOR APPLICATION DATA: including application
;; described below:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 197/243
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 34
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-07-936-421-16

Query Match 0.7%; Score 34; DB 1; Length 34;
Best Local Similarity 76.5%; Pred. No. 14;
Matches 26; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 2043 GGATGCCCTTTGTGGAAGTGTACGCCGCCAGCATG 2076
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Db 1 GGAUGCCUUUGGAAACUGACGCGCCCGCAUG 34

RESULT 9
US-07-936-421-21
;; Sequence 21, Application US/07936421
;; Patent No. 5750390
;; GENERAL INFORMATION:
;; APPLICANT: James D. Thompson
;; APPLICANT: Kenneth G. Draper
;; TITLE OF INVENTION: METHOD AND REAGENT FOR
;; TREATMENT OF DISEASES CAUSED
;; BY EXPRESSION OF THE BCL-2
;; TITLE OF INVENTION: GENE
;; NUMBER OF SEQUENCES: 22
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 611 West Sixth Street
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: USA
;; ZIP: 90017
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
;; SOFTWARE: WordPerfect (Version 5.1)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/936,421
;; FILING DATE: 19920826
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; PRIOR APPLICATION DATA: including application
;; described below:

none


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/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/894,784
/ FILING DATE: 15-DEC-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP96/00852
/ FILING DATE: 02-MAR-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: IL MI95 A 000420
/ FILING DATE: 03-MAR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Paul, John C.
/ REGISTRATION NUMBER: 30,413
/ REFERENCE/DOCKET NUMBER: 05999.0005-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 30 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ US-08-894-784-19

Query Match 0.6%; Score 30; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4256 GACCTGTTTCTTGAAGGTTTCTCGTCCC 4285
      |||||
Db 1 GACCTGTTTCTTGAAGGTTTCTCGTCCC 30

RESULT 14
US-08-894-784-23
/ Sequence 23, Application US/08894784
/ Patent No. 6005095
/ GENERAL INFORMATION:
/ APPLICANT: Capaccioli, Sergio
/ APPLICANT: Morelli, Susanna
/ APPLICANT: Nicolin, Angelo
/ TITLE OF INVENTION: ANTISENSE TRANSCRIPT ASSOCIATED TO TUMOR
/ TITLE OF INVENTION: CELLS HAVING A T(14;18) TRANSLOCATION AND
/ TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES USEFUL IN THE DIAGNOSIS AND
/ TITLE OF INVENTION: TREATMENT OF SAID TUMOR CELLS
/ NUMBER OF SEQUENCES: 49
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
/ ADDRESSEE: DUNNER, LLP
/ STREET: 1300 I Street, NW
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/894,784
/ FILING DATE: 15-DEC-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP96/00852
/ FILING DATE: 02-MAR-1996
/ PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: IL M195 A 000420
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, John C.
; REGISTRATION NUMBER: 30,413
; REFERENCE/DOCKET NUMBER: 05999.0005-000000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-894-784-23
; Query Match 0.6%; Score 30; DB 3; Length 30;
; Best Local Similarity 100.0%; Pred. No. 1.3e+02;
; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4256 GACCTTCTTCTTCAAGTTTCCTCGGCC 4285
Db 1 GACCTTCTTCTTCAAGTTTCCTCGGCC 30

RESULT 15
US-07-936-421-8
; Sequence 8, Application US/07936421
; Patent No. 5750390
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: TREATMENT OF DISEASES CAUSED
; TITLE OF INVENTION: BY EXPRESSION OF THE BCL-2
; TITLE OF INVENTION: GENE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/936.421
; FILING DATE: 19920826
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/243
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
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; TOPOLOGY: linear
US-07-936-421-8
; Query Match 0.6%; Score 28; DB 1; Length 28;
; Best Local Similarity 82.1%; Pred. No. 3.9e+02;
; Matches 23; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1729 CTTGTGTTCACCTGGCCCTCCGCCAAG 1756
Db 1 CCUGUGUCCACCGGCCGCCGCCAAG 28

RESULT 16
US-08-894-784-20/c
; Sequence 20, Application US/08894784
; Patent No. 6005095
; GENERAL INFORMATION:
; APPLICANT: Capaccioli, Sergio
; APPLICANT: Morelli, Susanna
; APPLICANT: Nicolin, Angelo
; TITLE OF INVENTION: ANTISENSE TRANSCRIPT ASSOCIATED TO TUMOR
; TITLE OF INVENTION: CELLS HAVING A T(14;18) TRANSLOCATION AND
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES USEFUL IN THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF SAID TUMOR CELLS
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; ADDRESSEE: DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,784
; FILING DATE: 15-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/00852
; FILING DATE: 02-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL M195 A 000420
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, John C.
; REGISTRATION NUMBER: 30,413
; REFERENCE/DOCKET NUMBER: 05999.0005-000000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-894-784-20
; Query Match 0.6%; Score 28; DB 3; Length 30;
; Best Local Similarity 100.0%; Pred. No. 4e+02;
; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4504 CTTCAAGGTTCTTCTGAAATGCAGTGGT 4531
Db 30 CTTCAAGGTTCTTCTGAAATGCAGTGGT 3

RESULT 17
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SEQUENCE CHARACTERISTICS:

DN Z CACACACACACACACAC

RESULT 30
US-08-222-177A-180
; Sequence 180, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd44rs
US-08-222-177A-180
Query Match 0.5%; Score 26.8; DB 1; Length 34;
Best Local Similarity 93.3%; Pred. No. 8.7e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2310 CACACACACACACACACACACACACA 2339
Db 1 CACACACACACACACACACACACACA 30
RESULT 31
US-08-222-177A-192
; Sequence 192, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd44rs
US-08-222-177A-180
Query Match 0.5%; Score 26.8; DB 1; Length 34;
Best Local Similarity 93.3%; Pred. No. 8.7e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2310 CACACACACACACACACACACACACA 2339
Db 1 CACACACACACACACACACACACACA 30
RESULT 32
US-08-222-177A-322
; Sequence 322, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 192:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd48rs
US-08-222-177A-192
Query Match 0.5%; Score 26.8; DB 1; Length 34;
Best Local Similarity 93.3%; Pred. No. 8.7e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2310 CACACACACACACACACACACACACA 2339
Db 2 CACACACACACACACACACACACACA 31
RESULT 32
US-08-222-177A-322
; Sequence 322, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 192:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd48rs
US-08-222-177A-192

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; TELEPHONE: (608) 831-2100
;
; TELEFAX: (608) 831-2106
;
;
; INFORMATION FOR SEQ ID NO: 322:
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; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
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; IMMEDIATE SOURCE:
;
; CLONE: mfd101rs
;
US-08-222-222-177A-322

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Query Match 0.5%; Score 26.8; DB 1; Length 34;
Best Local Similarity 93.3%; Pred. No. 8.7e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACAGACAGACACACACACA 2339
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 Db 2 CACACACACACACACACACACACA 31

RESULT 33
US-08-222-177A-77
; Sequence 77, Application US/08222177A
; Patent No. 5382979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:

Query Match 0.5%; Score 26.8; DB 1; Length 35;
Best Local Similarity 93.3%; Pred. No. 8.8e+02;
Matches 28; Conservative 0; Mismatches 2; Indels

QY 2310 CACACACAGACAGACACACACACA 2339
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 Db 1 CACACACACACACACACACACACACA 30

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RESULT 34
US-08-222-177A-189
; Sequence 189, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (GC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A

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Query Match      0.5%; Score 26.8; DB 1; Length 35;
Best Local Similarity 93.3%; Pred. No. 8.8e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY	2310	CACACACAGACAGACACACACACA	2339
Db	2	CACACACACACACACACACACACA	31

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RESULT 35
US-08-222-177A-104
; Sequence 104, Application US/08222177A
; Patent No. 5582379
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISM
; DATE OF INVENTION: (GC-DA)n. (GG-DA)n.
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens
;

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;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; IMMEDIATE SOURCE:
;; CLONE: mfd34rs
US-08-222-177A-152

Query Match 0.5%; Score 26.2; DB 1; Length 40;
Best Local Similarity 79.5%; Pred. No. 1.3e+03;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2311 ACACACACACACACACACACACACACACACAAATTAACA 2349
||||| ||| ||||||||| |||
Db 1 ACACACACATACACACACACACACACACACACACACACAC 39

RESULT 46

US-08-455-627-25
Sequence 25, Application US/08455627
Patent No. 5571677
;; GENERAL INFORMATION:
;; APPLICANT: Sergei M. Gryaznov
;; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
;; TITLE OF INVENTION: Connected Macromolecular Structures
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: Cooley Godward LLP
;; STREET: Five Palo Alto Square, 3000 El Camino Real
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94306-2155

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/455,627
;; FILING DATE: 31-MAY-1995

;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Nakamura, Jackie N.
;; REGISTRATION NUMBER: 35,966
;; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-843-5000
;; TELEFAX: 415-857-0663

;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 29 nucleotides
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-455-627-25

Query Match 0.5%; Score 25.8; DB 1; Length 29;
Best Local Similarity 93.1%; Pred. No. 1.4e+03;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACAC 2338
||||| ||| ||||||||| |||
Db 1 CACACACACACACACACACACACACACAC 29

RESULT 47

US-08-222-177A-80
Sequence 80, Application US/08222177A
Patent No. 5582979
;; GENERAL INFORMATION:
;; APPLICANT: Weber, James L.

;; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
;; TITLE OF INVENTION: (GC-DA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
;; NUMBER OF SEQUENCES: 460
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dewitt Ross & Stevens, S.C.
;; STREET: 8000 Excelsior Drive, Suite 401
;; CITY: Madison
;; STATE: Wisconsin
;; COUNTRY: USA
;; ZIP: 53717-1914
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/222,177A
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/341,562
;; FILING DATE: 21-APR-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sara, Charles S.
;; REGISTRATION NUMBER: 30,492
;; REFERENCE/DOCKET NUMBER: 09865.601
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (608) 831-2100
;; TELEFAX: (608) 831-2106
;; TELEX:

;; INFORMATION FOR SEQ ID NO: 80:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 29 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; IMMEDIATE SOURCE:
;; CLONE: mfd10rs
US-08-222-177A-80

Query Match 0.5%; Score 25.8; DB 1; Length 29;
Best Local Similarity 93.1%; Pred. No. 1.4e+03;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2311 ACACACACACACACACACACACACACACA 2339
||||| ||| ||||||||| |||
Db 1 ACACACACACACACACACACACACACACA 29

RESULT 48

US-08-222-177A-238
Sequence 238, Application US/08222177A
Patent No. 5582979
;; GENERAL INFORMATION:
;; APPLICANT: Weber, James L.

;; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
;; TITLE OF INVENTION: (GC-DA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
;; NUMBER OF SEQUENCES: 460
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dewitt Ross & Stevens, S.C.
;; STREET: 8000 Excelsior Drive, Suite 401
;; CITY: Madison
;; STATE: Wisconsin
;; COUNTRY: USA
;; ZIP: 53717-1914
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/222,177A

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;
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 238:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd65rs
; US-08-222-177A-238
;
; Query Match 0.5%; Score 25.8; DB 1; Length 29;
; Best Local Similarity 93.1%; Pred. No. 1.4e+03;
; Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 2310 CACACACACACACACACACACACAC 2338
; Db 1 CACACACACACACACACACACACAC 29
;
; RESULT 49
; US-08-689-856-25
; Sequence 25, Application US/08689856
; Patent No. 5830658
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
;
; QY 2310 CACACACACACACACACACACACAC 2338
; Db 1 CACACACACACACACACACACACAC 29
;
; RESULT 50
; US-08-222-177A-373
; Sequence 373, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dG-da)n.(dG-dt)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DeWitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 373:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd118rs
; US-08-222-177A-373
;
; Query Match 0.5%; Score 25.8; DB 1; Length 30;
; Best Local Similarity 93.1%; Pred. No. 1.4e+03;
; Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 2311 ACACACACACACACACACACACAC 2339
; Db 1 ACACACACACACACACACACACAC 29
;
; Search completed: May 31, 2003, 22:25:54
; Job time : 272 secs
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C 81	26.8	0.5	39	17	A2837376	A2837376	2M0132C10	C 154	23.8	0.5	33	17	A2473611	A2473611	1M0289001
C 82	26.8	0.5	40	17	A2319970	A2319970	1M0039K17	C 155	23.8	0.5	36	17	A2623245	A2623245	1M0460C15
C 83	26.8	0.5	40	17	A2338857	A2338857	1M0070A08	C 156	23.8	0.5	36	17	A2774711	A2774711	2M0004I17
C 84	26.8	0.5	40	17	A2587825	A2587825	1M0095F16	C 157	23.8	0.5	31	17	A2822976	A2822976	2M0096008
C 85	26.8	0.5	40	17	A2603138	A2603138	1M0422G15	C 158	23.6	0.5	31	17	A2399554	A2399554	1M0165019
C 86	26.8	0.5	40	17	A2808181	A2808181	2M0071A18	C 159	23.6	0.5	31	17	A2432709	A2432709	1M0218C16
C 87	26.8	0.5	40	17	A2819018	A2819018	2M0089I19	C 160	23.6	0.5	33	17	A2514079	A2514079	1M0360F07
C 88	26.6	0.5	34	17	A2438581	A2438581	1M0228D16	C 161	23.6	0.5	34	17	A2483866	A2483866	1M0310N01
C 89	26.6	0.5	38	17	A2983391	A2983391	2M0264I05	C 162	23.6	0.5	34	17	A2622092	A2622092	1M0455H07
C 90	26.4	0.5	40	17	A2513013	A2513013	1M0358M21	C 163	23.6	0.5	34	17	A2875700	A2875700	2M0190D19
C 91	26.2	0.5	33	17	A2626646	A2626646	1M0467E06	C 164	23.6	0.5	35	17	A2580498	A2580498	1M0368I15
C 92	26.2	0.5	36	17	A2488673	A2488673	1M0322E18	C 165	23.6	0.5	35	17	A2960947	A2960947	2M0229M11
C 93	26.2	0.5	39	17	A2480184	A2480184	1M0301E04	C 166	23.6	0.5	38	17	A2426925	A2426925	1M0208E11
C 94	26.2	0.5	40	17	A2781595	A2781595	2M0021P06	C 167	23.6	0.5	39	17	A2588176	A2588176	1M0396M11
C 95	25.8	0.5	29	17	A2315179	A2315179	1M0032K18	C 168	23.4	0.5	38	17	A2424085	A2424085	1M0230B05
C 96	25.8	0.5	29	17	A2414401	A2414401	1M0188M13	C 169	23.2	0.5	37	17	A2420346	A2420346	1M0198G12
C 97	25.8	0.5	30	17	A2458713	A2458713	1M0263L02	C 170	23.2	0.5	37	17	A2484142	A2484142	1M0310E24
C 98	25.8	0.5	30	17	A2497897	A2497897	1M0334K20	C 171	23	0.5	33	17	A2345522	A2345522	1M0080L05
C 99	25.8	0.5	30	17	A2989744	A2989744	2M0273N10	C 172	23	0.5	39	17	A2826077	A2826077	2M0263H11
C 100	25.8	0.5	31	17	A2628068	A2628068	1M0476P22	C 173	23	0.5	39	17	A2479725	A2479725	1M0101A07
C 101	25.8	0.5	35	17	A2483942	A2483942	1M0309H20	C 174	23	0.5	40	17	A2800091	A2800091	2M0057K22
C 102	25.8	0.5	37	17	A2456482	A2456482	1M0259P11	C 175	23	0.5	26	17	A2307889	A2307889	1M0010L18
C 103	25.8	0.5	37	17	A2857946	A2857946	2M0162M19	C 176	22.8	0.4	26	17	A2345505	A2345505	1M0080H01
C 104	25.8	0.5	40	17	A2837355	A2837355	2M0132004	C 177	22.8	0.4	26	17	A2494537	A2494537	1M0329D24
C 105	25.6	0.5	40	17	A2328984	A2328984	1M0053H01	C 178	22.8	0.4	26	17	A2503652	A2503652	1M0343F01
C 106	25.2	0.5	30	17	A2635862	A2635862	1M0493C04	C 179	22.8	0.4	26	17	A2795803	A2795803	2M0051P11
C 107	25.2	0.5	31	17	A2659684	A2659684	1M0537C17	C 180	22.8	0.4	26	17	A2806004	A2806004	2M0067H16
C 108	25.2	0.5	32	17	A2496969	A2496969	1M0333E07	C 181	22.8	0.4	26	17	A2975568	A2975568	2M0250L12
C 109	25.2	0.5	32	17	A2661921	A2661921	1M0540B17	C 182	22.8	0.4	26	17	A2329433	A2329433	1M0053K11
C 110	25.2	0.5	34	17	A2509672	A2509672	1M0352A18	C 183	22.8	0.4	27	17	A2788874	A2788874	2M0036H16
C 111	25.2	0.5	35	17	A26313057	A26313057	1M0441C17	C 184	22.8	0.4	27	17	A2801217	A2801217	2M0059P03
C 112	25.2	0.5	36	17	A2968276	A2968276	2M0240K02	C 185	22.8	0.4	29	17	A2866837	A2866837	2M0170201
C 113	25.2	0.5	37	17	A2875282	A2875282	2M0189A20	C 186	22.8	0.4	29	17	A2807584	A2807584	2M0070H04
C 114	25.2	0.5	40	17	A2974885	A2974885	2M0249P09	C 187	22.6	0.4	29	17	A2860659	A2860659	2M0166F14
C 115	25.2	0.5	39	17	A2397262	A2397262	1M0162I12	C 188	22.6	0.4	30	17	A2371116	A2371116	1M0122J05
C 116	24.8	0.5	28	17	A2330730	A2330730	1M0056C11	C 189	22.6	0.4	32	17	A2797258	A2797258	2M0053F22
C 117	24.8	0.5	28	17	A2443611	A2443611	1M0238N03	C 190	22.6	0.4	35	17	A2477397	A2477397	1M0296D19
C 118	24.8	0.5	28	17	A2467078	A2467078	1M0278C15	C 191	22.6	0.4	32	17	A2833699	A2833699	2M0097G23
C 119	24.8	0.5	28	17	A2514383	A2514383	1M0361G05	C 192	22.4	0.4	32	17	A2338269	A2338269	1M0096Q17
C 120	24.8	0.5	28	17	A2644345	A2644345	1M0508E16	C 193	22.4	0.4	32	17	A2848648	A2848648	2M0149B14
C 121	24.8	0.5	28	17	A2648665	A2648665	1M0517J18	C 194	22.4	0.4	37	17	A2595102	A2595102	1M0407F03
C 122	24.8	0.5	28	17	A2649197	A2649197	1M0518E11	C 195	22.4	0.4	37	17	A2442363	A2442363	1M0236B17
C 123	24.8	0.5	28	17	A2777903	A2777903	2M0012D16	C 196	22.2	0.4	28	17	A2625192	A2625192	1M0464J22
C 124	24.8	0.5	28	17	A2812746	A2812746	2M0079H07	C 197	22.2	0.4	30	17	A2640238	A2640238	1M0502H10
C 125	24.8	0.5	29	17	A2786559	A2786559	2M0032D12	C 198	22	0.4	38	17	A2643646	A2643646	1M0507A17
C 126	24.8	0.5	30	17	A2412174	A2412174	1M0185H01	C 199	22	0.4	39	17	A263038	A263038	1M0476N17
C 127	24.8	0.5	30	17	A2579506	A2579506	1M0367E06	C 200	22	0.4	25	17	A2339866	A2339866	1M0071H01
C 128	24.8	0.5	32	17	A2829236	A2829236	2M0106H16	C 201	22	0.4	25	17	A2404057	A2404057	1M0172D10
C 129	24.8	0.5	34	17	A2807557	A2807557	2M0070B06	C 202	22	0.4	25	17	A2769673	A2769673	1M0570D12
C 130	24.6	0.5	31	17	A2841151	A2841151	1M0406H16	C 203	22	0.4	25	17	A2771881	A2771881	1M0574F23
C 131	24.6	0.5	32	17	A2304813	A2304813	1M0095L18	C 204	22	0.4	26	17	A2419877	A2419877	1M0196N03
C 132	24.6	0.5	34	9	A1539675	A1539675	tp71f03.x	C 205	21.8	0.4	26	17	A2646850	A2646850	1M0513L06
C 133	24.6	0.5	35	17	A2491991	A2491991	1M0325C24	C 206	21.8	0.4	26	17	A2830551	A2830551	2M0109C19
C 134	24.6	0.5	39	17	A2511942	A2511942	1M0357O08	C 207	21.8	0.4	33	17	A2766046	A2766046	1M0563N18
C 135	24.4	0.5	35	17	A2512195	A2512195	1M0357O04	C 208	21.8	0.4	33	17	A2799903	A2799903	2M0057G08
C 136	24.2	0.5	29	17	A2663681	A2663681	1M0453M21	C 209	21.8	0.4	33	17	A2826970	A2826970	2M0103006
C 137	24.2	0.5	29	17	A2774254	A2774254	2M0003L23	C 210	21.8	0.4	34	17	A2656447	A2656447	1M0532C02
C 138	24.2	0.5	30	17	A2425112	A2425112	1M0205I01	C 211	21.8	0.4	38	12	BG778513	BG778513	60266730
C 139	24.2	0.5	30	17	A2815799	A2815799	2M0084F24	C 212	21.8	0.4	31	17	A2346705	A2346705	1M0082M02
C 140	24.2	0.5	30	17	TAYAL12P	TAYAL12P	T. brucei	C 213	21.8	0.4	37	17	A2666510	A2666510	1M0548M11
C 141	24.2	0.5	31	17	A2440652	A2440652	1M0231N14	C 214	21.6	0.4	38	17	A2490125	A2490125	1M0333M11
C 142	24.2	0.5	31	17	A2494653	A2494653	1M0330K03	C 215	21.8	0.4	38	17	AZ500372	AZ500372	1M0333M11
C 143	24.2	0.5	31	17	A2803691	A2803691	2M0064A17	C 216	21.8	0.4	31	17	A2465284	A2465284	1M0275B10
C 144	23.8	0.5	27	17	A2342492	A2342492	1M0075004	C 217	21.6	0.4	40	17	AZ781134	AZ781134	2M0019B09
C 145	23.8	0.5	27	17	A2435344	A2435344	1M0222K17	C 218	21.6	0.4	37	17	AZ814562	AZ814562	2M0082A22
C 146	23.8	0.5	27	17	A2583081	A2583081	1M0376L16	C 219	21.6	0.4	37	17	AZ784558	AZ784558	2M0027G15
C 147	23.8	0.5	27	17	A2638238	A2638238	1M0498H05	C 220	21.6	0.4	38	17	AU266086	AU266086	AU266086
C 148	23.8	0.5	27	17	AZ758321	AZ758321	1M0550G18	C 221	21.6	0.4	38	17			
C 149	23.8	0.5	27	17	AZ981811	AZ981811	2M0262D23	C 222	21.4	0.4	31	17			
C 150	23.8	0.5	28	17	AZ366137	AZ366137	1M0115B21	C 223	21.4	0.4	34	17			
C 151	23.8	0.5	28	17	AZ405219	AZ405219	1M0173N21	C 224	21.4	0.4	37	17			
C 152	23.8	0.5	28	17	AZ782113	AZ782113	2M0022N03	C 225	21.4	0.4	38	9			

226	21.4	0.4	39	17	AZ861762	AZ861762	2M0168J10	C 299	20.4	0.4	38	17	AZ861891	AZ861891	2M0168H15
227	21.4	0.4	39	17	AZ949919	AZ949919	2M0213B16	300	20.4	0.4	38	17	AZ863994	AZ863994	2M0173B22
228	21.4	0.4	39	17	AZ949919	AL764506	Arabidops	301	20.4	0.4	38	17	AZ863994	AZ863994	2M0173B22
229	21.4	0.4	39	17	DR11A19T	AL734670	Danio rer	302	20.4	0.4	38	17	AZ863994	AZ863994	2M0173B22
230	21.4	0.4	40	9	AI198940	AI198940	qf66f09.x	C 303	20.4	0.4	39	17	AZ863994	AZ863994	2M0173B22
231	21.4	0.4	40	17	AZ369493	AZ369493	1M0120B11	C 304	20.4	0.4	39	17	AZ863994	AZ863994	2M0173B22
232	21.4	0.4	40	17	AZ897967	AZ897967	2M0037D20	305	20.4	0.4	39	17	AZ863994	AZ863994	2M0173B22
233	21.4	0.4	40	17	AZ897967	AZ897967	2M0037D20	306	20.4	0.4	39	17	AZ863994	AZ863994	2M0173B22
234	21.2	0.4	26	17	AZ766495	AZ766495	1M0564D08	C 307	20.4	0.4	9	AA452094	AA452094	zx30h08.s	
235	21.2	0.4	26	17	AZ766495	AZ766495	1M0564D08	C 308	20.4	0.4	14	D21037	D21037	HUMG02020	
236	21.2	0.4	26	17	AZ646963	AZ646963	2M0153C13	309	20.2	0.4	25	AZ451588	AZ451588	1M0251105	
237	21.2	0.4	27	17	AZ946507	AZ946507	2M0208O18	310	20.2	0.4	25	AZ780500	AZ780500	2M0017J19	
238	21.2	0.4	33	17	TA34G07P	AL452996	T. brucei	C 311	20.2	0.4	26	AZ467063	AZ467063	1M0278O07	
239	21.2	0.4	34	17	AZ322675	AZ322675	1M0432D10	C 312	20.2	0.4	33	12	BE866705	BE866705	601507961
240	21.2	0.4	34	17	AZ771845	AZ771845	1M0574M14	C 313	20.2	0.4	33	12	AZ373632	AZ373632	1M0126B22
241	21.2	0.4	34	17	TA68D10P	AL457502	T. brucei	C 314	20.2	0.4	33	17	AZ627977	AZ627977	1M0476L03
242	21.2	0.4	40	12	BF213125	BF213125	601844961	C 315	20.2	0.4	34	10	AV857665	AV857665	AV857665
243	21.2	0.4	40	17	AZ410396	AZ410396	1M0182N11	316	20.2	0.4	34	17	AZ514577	AZ514577	1M0361P11
244	21	0.4	30	17	AZ809317	AZ809317	2M0073F14	C 317	20.2	0.4	34	17	AZ645914	AZ645914	1M0511K08
245	21	0.4	36	9	AL639933	AL639933	AL639933	C 318	20.2	0.4	35	17	AZ838204	AZ838204	2M0133K17
246	21	0.4	37	17	AZ654776	AZ654776	1M0529M10	319	20.2	0.4	36	17	AZ462645	AZ462645	1M0269M12
247	21	0.4	38	17	AZ402445	AZ402445	1M0169D13	320	20.2	0.4	36	17	AZ766476	AZ766476	1M0564P01
248	21	0.4	38	17	AZ655948	AZ655948	1M0531N12	C 321	20.2	0.4	36	17	AL763948	AL763948	Arabidops
249	21	0.4	38	17	AZ949765	AZ949765	2M0213D06	C 322	20.2	0.4	37	17	AZ498469	AZ498469	1M0335L17
250	21	0.4	39	17	BH789389	BH789389	SALK_0191	323	20.2	0.4	37	17	TA51G08Q	TA51G08Q	T. brucei
251	21	0.4	39	17	AL757684	AL757684	Arabidops	324	20.2	0.4	39	10	AW248768	AW248768	2820919.3
252	21	0.4	40	2	HSM002456	AL038117	Homo sapi	325	20.2	0.4	40	2	HSM003149	HSM003149	AL038673
253	21	0.4	40	17	TA115808P	AL452822	T. brucei	326	20.2	0.4	40	9	AI697142	AI697142	1M0564B09.x
254	20.8	0.4	24	17	AZ419602	AZ419602	1M0196L12	C 327	20	0.4	29	14	N53413	N53413	2M025606.s1
255	20.8	0.4	24	17	AZ446429	AZ446429	1M0242A24	C 328	20	0.4	29	17	AZ8266631	AZ8266631	2M0102E22
256	20.8	0.4	24	17	AZ621455	AZ621455	1M0454K11	C 329	20	0.4	31	17	TA338C10P	TA338C10P	AL493149
257	20.8	0.4	24	17	AZ807762	AZ807762	2M0070O14	C 330	20	0.4	34	17	AZ475648	AZ475648	1M0293G05
258	20.8	0.4	24	17	AZ813106	AZ813106	2M0080A16	C 331	20	0.4	34	17	AZ990901	AZ990901	2M0274N14
259	20.8	0.4	24	17	AZ846178	AZ846178	2M0146F14	C 332	20	0.4	36	17	AZ337595	AZ337595	1M0068O17
260	20.8	0.4	24	17	TA163H11P	AL472248	T. brucei	333	20	0.4	36	17	AZ623038	AZ623038	1M0460L13
261	20.8	0.4	25	17	AZ345553	AZ345553	1M0080E16	334	20	0.4	36	17	AZ629871	AZ629871	1M0483E08
262	20.8	0.4	25	17	AZ465273	AZ465273	1M0275P01	335	20	0.4	36	17	AZ643259	AZ643259	1M0506G06
263	20.8	0.4	25	17	AZ467470	AZ467470	1M0278E21	336	20	0.4	36	17	AZ772448	AZ772448	1M0583O18
264	20.8	0.4	25	17	AZ762101	AZ762101	1M0556K17	337	20	0.4	36	17	AZ777125	AZ777125	2M0011O18
265	20.8	0.4	33	17	TA245A09Q	AL482142	T. brucei	C 338	20	0.4	36	17	AZ777975	AZ777975	2M0012F19
266	20.8	0.4	33	17	TA356C09P	AL497114	T. brucei	339	20	0.4	36	17	AZ799331	AZ799331	2M0056D07
267	20.8	0.4	34	9	AI122781	AI122781	qa48g10.x	340	20	0.4	36	17	AZ806045	AZ806045	2M0067P17
268	20.8	0.4	34	10	AW251037	AW251037	2821413.3	341	20	0.4	36	17	AZ829267	AZ829267	2M0106O14
269	20.8	0.4	35	17	AZ639148	AZ639148	1M0499M21	342	20	0.4	36	17	AZ847638	AZ847638	2M0148K14
270	20.8	0.4	35	17	AZ663471	AZ663471	1M0543D09	343	20	0.4	36	17	AZ873086	AZ873086	2M0186M07
271	20.8	0.4	37	9	AA873697	AA873697	ob36g11.s	C 344	20	0.4	37	9	AA903696	AA903696	ok54h06.s
272	20.8	0.4	40	17	AZ330731	AZ330731	1M0056C12	345	20	0.4	37	9	AI129902	AI129902	qc41b07.x
273	20.8	0.4	40	17	AZ556548	AZ556548	1M0532H11	346	20	0.4	37	9	AA18459	AA18459	zv92h04.r
274	20.8	0.4	40	17	AZ761020	AZ761020	1M0555E08	C 347	20	0.4	37	17	AZ311322	AZ311322	1M0036N11
275	20.8	0.4	40	17	AZ813380	AZ813380	2M0081D06	348	20	0.4	37	17	AZ459123	AZ459123	1M0263D16
276	20.8	0.4	40	17	AZ952893	AZ952893	2M0217G24	349	20	0.4	37	17	AZ761163	AZ761163	1M0555P18
277	20.6	0.4	27	9	AU264164	AU264164	AU264164	350	20	0.4	37	17	AZ771220	AZ771220	1M0573A15
278	20.6	0.4	28	17	AZ345426	AZ345426	1M0080A09	351	20	0.4	37	17	AZ853189	AZ853189	2M0156D13
279	20.6	0.4	28	17	AZ466703	AZ466703	1M0277N06	352	20	0.4	37	17	AZ997433	AZ997433	2M0284A01
280	20.6	0.4	31	14	RI4943	RI4943	Yf94g04.r1	353	20	0.4	37	17	TA226A08Q	TA226A08Q	T. brucei
281	20.6	0.4	35	17	AZ317100	AZ317100	1M0035E01	354	20	0.4	38	17	AZ589726	AZ589726	1M0398I24
282	20.6	0.4	35	17	AZ389253	AZ389253	1M0149K07	355	20	0.4	38	17	AZ657455	AZ657455	1M0533H08
283	20.6	0.4	35	17	AZ581591	AZ581591	1M0370O23	C 356	20	0.4	39	9	AL636986	AL636986	AL636986
284	20.6	0.4	36	17	AZ588848	AZ588848	1M0397M24	C 357	20	0.4	39	9	AU265743	AU265743	AU265743
285	20.6	0.4	36	17	AZ764529	AZ764529	1M0560L17	C 358	20	0.4	39	9	AU270022	AU270022	AU270022
286	20.6	0.4	36	17	TA270H08P	AL484129	T. brucei	C 359	20	0.4	39	13	BI694035	BI694035	603342221
287	20.6	0.4	37	17	AZ369295	AZ369295	1M0119M13	360	20	0.4	39	17	CNS004NT	CNS004NT	AL054298
288	20.4	0.4	30	10	BE539470	BE539470	601060134	361	20	0.4	39	17	TA116F09P	TA116F09P	AL462533
289	20.4	0.4	31	17	AZ402199	AZ402199	1M0169H20	C 362	20	0.4	39	17	TA200E07Q	TA200E07Q	AL477832
290	20.4	0.4	31	17	AZ775768	AZ775768	2M0008F23	C 363	20	0.4	39	17	TA285C10P	TA285C10P	AL477832
291	20.4	0.4	34	17	AZ774656	AZ774656	2M0004K10	364	20	0.4	40	2	HSM002701	HSM002701	AL1038357
292	20.4	0.4	35	9	AL787430	AL787430	AL787430	365	20	0.4	40	13	BG976639	BG976639	602846941
293	20.4	0.4	37	17	AZ340720	AZ340720	1M0072022	C 366	20	0.4	40	17	AZ466333	AZ466333	1M0276P22
294	20.4	0.4	38	10	AW332997	AW332997	S16A3 AGS	367	19.8	0.4	42	17	AZ328763	AZ328763	1M0052L12
295	20.4	0.4	38	17	AZ462853	AZ462853	1M0271D22	C 368	19.8	0.4	23	17	AZ483624	AZ483624	1M0309C01
296	20.4	0.4	38	17	AZ512402	AZ512402	1M0357H20	369	19.8	0.4	23	17	AZ637290	AZ637290	1M0496O05
297	20.4	0.4	38	17	AZ764657	AZ764657	1M0561J11	370	19.8	0.4	23	17	AZ789907	AZ789907	2M0038G13
298	20.4	0.4	38	17	AZ777129	AZ777129	2M0011P18	371	19.8	0.4	23	17	AZ828969	AZ828969	2M0106O13

372	19.8	0.4	23	17	AZ829195	2M0106M12	445	19.2	0.4	27	17	AZ827502	AZ827502	2M0103020
373	19.8	0.4	24	17	AZ647335	1M0513J15	446	19.2	0.4	30	17	AZ790051	AZ790051	2M0038P15
374	19.8	0.4	25	17	AZ766498	1M0564E08	447	19.2	0.4	32	9	AL587570	AL587570	AL587570
375	19.8	0.4	31	17	AZ861612	2M0168P16	448	19.2	0.4	32	17	AZ316355	AZ316355	1M0034H10
376	19.8	0.4	32	2	HS0003156	AL038680	c 449	19.2	0.4	32	17	AZ764538	AZ764538	1M0560N21
377	19.8	0.4	33	9	AU013658	AU013658	450	19.2	0.4	33	9	AU258912	AU258912	AU258912
378	19.8	0.4	34	10	AV674152	AV674152	451	19.2	0.4	33	9	AU269499	AU269499	AU269499
379	19.8	0.4	34	10	AW334249	AW334249	452	19.2	0.4	33	17	AZ404047	AZ404047	1M0172A10
380	19.8	0.4	34	17	AZ345610	1M0080C24	453	19.2	0.4	33	17	AZ484644	AZ484644	1M0311H13
381	19.8	0.4	35	12	BE894837	BE894837	454	19.2	0.4	33	17	AZ620923	AZ620923	1M0453P17
382	19.8	0.4	35	17	AZ636745	1M0495F14	c 455	19.2	0.4	33	17	AZ793186	AZ793186	2M0048A13
383	19.8	0.4	35	17	AZ845779	2M0145B13	456	19.2	0.4	33	17	TA95A01P	TA95A01P	AL458992
384	19.8	0.4	37	9	AI687908	AI687908	c 457	19.2	0.4	34	12	BG612023	BG612023	602613924
385	19.8	0.4	38	17	TA264B08P	TA264B08P	c 458	19.2	0.4	35	17	AZ351309	AZ351309	1M0089K13
386	19.8	0.4	40	9	AU263859	AU263859	c 459	19.2	0.4	35	17	AZ774099	AZ774099	2M0003F08
387	19.8	0.4	40	9	AU264483	AU264483	c 460	19.2	0.4	36	12	BE894682	BE894682	601435925
388	19.8	0.4	40	14	C00202	C00202	461	19.2	0.4	36	17	AZ456524	AZ456524	1M0253I18
389	19.8	0.4	40	17	AZ793917	AZ793917	462	19.2	0.4	37	9	AI267817	AI267817	AZ267817
390	19.6	0.4	26	17	AZ774981	2M0004D22	c 463	19.2	0.4	37	13	BJ054011	BJ054011	BJ054011
391	19.6	0.4	26	17	TA70E08Q	TA70E08Q	464	19.2	0.4	37	17	TA15E07P	TA15E07P	TA15E07P
392	19.6	0.4	27	17	AZ404479	1M0172F18	c 465	19.2	0.4	37	17	TA256H06P	TA256H06P	TA256H06P
393	19.6	0.4	27	17	TA287F07P	TA287F07P	466	19.2	0.4	38	9	AU269612	AU269612	AU269612
394	19.6	0.4	31	9	AI364457	AI364457	c 467	19.2	0.4	38	9	AU271278	AU271278	AU271278
395	19.6	0.4	31	9	AI973247	AI973247	c 468	19.2	0.4	39	9	BH789389	BH789389	BH789389
396	19.6	0.4	34	10	AW698832	AW698832	469	19.2	0.4	39	17	AI424339	AI424339	AI424339
397	19.6	0.4	35	12	BF338797	BF338797	c 470	19.2	0.4	40	12	BG772038	BG772038	602721673
398	19.6	0.4	35	17	AZ321115	1M0041H02	c 471	19.2	0.4	40	13	BI668945	BI668945	603294924
399	19.6	0.4	35	17	BH000551	2M0288F03	472	19.2	0.4	40	17	AZ335687	AZ335687	1M0065D23
400	19.6	0.4	36	13	BI761940	603048F72	c 473	19.2	0.4	40	17	AZ391073	AZ391073	1M0152I24
401	19.6	0.4	36	17	AZ627849	1M0474I13	c 474	19.2	0.4	40	17	BH791898	BH791898	SAUK_0619
402	19.6	0.4	37	9	AI018534	AI018534	c 475	19.2	0.4	27	17	AZ325394	AZ325394	1M0047F17
403	19.6	0.4	37	9	AI037939	AI037939	c 476	19.2	0.4	28	17	AZ781477	AZ781477	1M0019H24
404	19.6	0.4	37	12	BG430173	BG430173	c 477	19.2	0.4	28	17	AZ961930	AZ961930	2M0230L03
405	19.6	0.4	37	12	AZ442522	1M0236D07	c 478	19.2	0.4	30	9	AU266910	AU266910	AU266910
406	19.6	0.4	38	12	BF525501	602069S92	c 479	19.2	0.4	30	17	AZ386218	AZ386218	1M0145M04
407	19.6	0.4	38	12	BF526154	602071057	480	19.2	0.4	32	14	RI6114	RI6114	ya51f03.s2
408	19.6	0.4	38	17	AZ484773	1M0311B02	c 481	19.2	0.4	34	9	AL683575	AL683575	tw52b11.x
409	19.6	0.4	38	17	AZ776539	2M0010D15	c 482	19.2	0.4	35	9	AL632985	AL632985	AL632985
410	19.6	0.4	39	9	AU264049	AU264049	483	19.2	0.4	35	17	AZ609583	AZ609583	1M0434L13
411	19.6	0.4	39	12	BG287495	BG287495	484	19.2	0.4	35	17	AZ764499	AZ764499	1M0560K05
412	19.6	0.4	40	9	AL804001	AL804001	c 485	19.2	0.4	35	17	AZ764535	AZ764535	1M0560A22
413	19.6	0.4	40	12	BG166502	602339795	c 486	19.2	0.4	35	17	AZ784082	AZ784082	2M0028E04
414	19.6	0.4	40	17	AZ789792	2M0037J19	487	19.2	0.4	35	17	AZ817073	AZ817073	2M0086D07
415	19.4	0.4	21	17	AZ626965	1M0467E15	488	19.2	0.4	35	17	AZ831930	AZ831930	2M0110E21
416	19.4	0.4	27	17	AZ763599	1M0559E08	489	19.2	0.4	35	17	AZ858898	AZ858898	2M0164H14
417	19.4	0.4	29	17	AZ666737	1M0549O06	490	19.2	0.4	35	17	AZ861607	AZ861607	2M0168P11
418	19.4	0.4	29	17	AZ825156	2M0100N08	c 491	19.2	0.4	35	17	AZ967442	AZ967442	2M0238F20
419	19.4	0.4	30	17	AZ412824	1M0186F02	492	19.2	0.4	35	17	AZ969917	AZ969917	2M0242D20
420	19.4	0.4	30	17	AZ486010	1M0313F15	c 493	19.2	0.4	35	17	AL752534	AL752534	Arabiadops
421	19.4	0.4	30	17	TA226G05P	TA226G05P	c 494	19.2	0.4	36	13	BI078346	BI078346	602874206
422	19.4	0.4	31	9	AI677781	AI677781	c 495	19.2	0.4	36	17	AZ970687	AZ970687	2M0243I23
423	19.4	0.4	31	17	AZ486763	1M0315A11	c 496	19.2	0.4	37	9	AA934710	AA934710	oo72a03.s
424	19.4	0.4	31	17	AZ967197	2M0238H01	c 497	19.2	0.4	37	9	AL587823	AL587823	AL587823
425	19.4	0.4	32	17	AZ314322	1M0031N05	c 498	19.2	0.4	37	17	AZ623276	AZ623276	1M0460M16
426	19.4	0.4	32	17	AZ451231	1M0250I05	499	19.2	0.4	38	10	AW333985	AW333985	S28H9 AGS
427	19.4	0.4	33	17	AZ586664	1M0392N08	c 500	19.2	0.4	38	17	AL763877	AL763877	Arabiadops
428	19.4	0.4	33	17	AZ661578	1M0540C08								
429	19.4	0.4	34	17	AZ476549	1M0295P24								
430	19.4	0.4	34	17	AL510095	1M0354B20								
431	19.4	0.4	35	9	AL641482	AL641482								
432	19.4	0.4	35	10	AV966617	AV966617								
433	19.4	0.4	36	17	AZ328537	AZ328537								
434	19.4	0.4	36	17	TA270G05P	TA270G05P								
435	19.4	0.4	37	17	AZ758338	1M0550J17								
436	19.4	0.4	37	17	DR11K9T	DR11K9T								
437	19.4	0.4	38	17	AZ600409	1M0418A07								
438	19.4	0.4	39	2	HS0002488	HS0002488								
439	19.4	0.4	39	14	D25655	D25655								
440	19.4	0.4	40	2	HS0001841	HS0001841								
441	19.4	0.4	40	9	AL638703	AL638703								
442	19.2	0.4	25	17	AZ459694	AZ459694								
443	19.2	0.4	25	17	AZ506209	AZ506209								
444	19.2	0.4	27	17	AZ784556	AZ784556								

ALIGNMENTS

39 bp DNA linear

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ALIGNMENTS

RESULT 1
AZ813889/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ813889
2M0081B23F Mouse 10kb plasmid UGCLM library Mus musculus genomic clone UGCLM0081B23 F, DNA sequence.
AZ813889
GI:12983785
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

39 bp DNA linear
GSS 20-FEB-2001

REFERENCE
AUTHORS

1 (bases 1 to 39)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0081 row: B column: 23

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 39.

Location/Qualifiers

1..39

FEATURES
source

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M081B23"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

5 a 0 c 16 g 18 t

Query Match 0.6%; Score 31; DB 17; Length 39;
Best Local Similarity 87.2%; Pred. No. 8.5e+04;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACATTAAC 2348

Db 39 CACACACACACACACACACACACACTTACATTAC 1

RESULT 2
AZ647581/c

LOCUS

AZ647581 37 bp DNA linear GSS 14-DEC-2000
DEFINITION M0514J14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0514J14 F, DNA sequence.

ACCESSION

AZ647581

VERSION

AZ647581.1 GI:11779189

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 37)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0514 row: J column: 14

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 37.

Location/Qualifiers

1..37

FEATURES
source

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0514J14"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 18 g 19 t

ORIGIN

Query Match 0.6%; Score 29.2; DB 17; Length 37;
Best Local Similarity 91.2%; Pred. NO. 2.1e+05;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACAA 2343

Db 36 CACACACACACACACACACACACACACACAA 3

RESULT 3

AZ832583

LOCUS

AZ832583 35 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0113N06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0113N06 F, DNA sequence.

ACCESSION

AZ832583

VERSION

AZ832583.1 GI:13002491

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE	1 (bases 1 to 36)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: rdunne@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0032 row: K column: 19 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 36.

FEATURES	source
Location/Qualifiers	
1..36	
/organism="Mus musculus"	
/strain="C57BL/6J"	
/db_xref="taxon:10090"	
/clone="UUGCLM0032K19"	
/clone.lib="Mouse 10kb plasmid UUGCLM library"	
/sex="Male"	
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"	
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
0 a	14 g 21 t
BASE COUNT	

REFERENCE	1 (bases 1 to 35)
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10Kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT, 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0113 row: N column: 06 Seq primer: CGTTGTAACGACGCCAGT Class: plasmid ends High quality sequence stop: 35

```

FEATURES
source
    mag. quality=90.00;
    Location/Qualifiers
        .
        ..35
        /organism="Mus musculus"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC2M0113N06"
        /clone_lib="Mouse 10kb plasmid UUGc1m library"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57Bl/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g1147321141gb1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
        ..15 c      0 g      2 t
        18 a

```

[illegible]

REFERENCE
AUTHORS

1 (bases 1 to 37)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0082 row: 0 column: 09

Seq primer: CGTTGTTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 37.

Location/Qualifiers

1. .37

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M082009"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT 19 a 17 c 0 g 1 t

ORIGIN

Query Match

Best Local Similarity 0.6%; Score 28.6; DB 17; Length 37;

Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACAAAT 2344

Db 3 CACACACACACACACACACACACACACAAAT 37

RESULT 6

AZ389462/c

LOCUS

DEFINITION IM0150D06F Mouse 10kb plasmid UUC1M library Mus musculus genomic

clone UUC1M0150D06 F, DNA sequence.

ACCESSION AZ389462

VERSION AZ389462.1 GI:10503170

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 39)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0150 row: D column: 06

Seq primer: CGTTGTTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 39.

Location/Qualifiers

1. .39

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0150D06"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT 1 a 0 c 18 g 20 t

ORIGIN

Query Match

Best Local Similarity 0.6%; Score 28.4; DB 17; Length 39;

Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACAATAA 2347

Db 39 CACACACACACACACACACACACACACAATAA 2

RESULT 7

AZ304764/c

LOCUS

DEFINITION IM0005A14F Mouse 10kb plasmid UUC1M library Mus musculus genomic

clone UUC1M0005A14 F, DNA sequence.

ACCESSION AZ304764

VERSION AZ304764.1 GI:10341104

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 34)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0005 row: A column: 14

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 34.

FEATURES

Location/Qualifiers

Source

1..34
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0005A14"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

Query Match 0.6%; Score 28.2; DB 17; Length 34;
Best Local Similarity 90.9%; Pred. No. 3.4e+05;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2311 ACACACACACACACACACACACACACACACAA 2343

||||||| ||| ||||||||| |||||
Db 34 ACACACACACACACACACACACACACACACAA 2

RESULT 8

AZ803581/c

LOCUS

DEFINITION 2M0064L05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0064L05 F, DNA sequence.

ACCESSION AZ803581

VERSION AZ803581.1

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 38)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0064 row: L column: 05

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 38.

FEATURES

Location/Qualifiers

Source

1..38
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0064L05"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

Query Match 0.6%; Score 28; DB 17; Length 38;
Best Local Similarity 86.1%; Pred. No. 3.7e+05;
Matches 31; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACACATT 2345

||||||| ||| ||||||||| |||||
Db 38 CACACACACACACACACACACACACACAACT 3

RESULT 9

AZ638769/c

LOCUS

DEFINITION 1M0498B20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0498B20 R, DNA sequence.

ACCESSION AZ638769

VERSION AZ638769.1

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 35)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0089 row: G column: 02

Seq primer: CACACAGGAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 35.

Location/Qualifiers

1. .35

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0089G02"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

0 a 0 c 17 g 18 t

Query Match

0.5%; Score 27.8; DB 17; Length 35;

Best Local Similarity 93.5%; Pred. No. 4.1e+05;

Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACAA 2340

|||||

Db 31 CACACACACACACACACACACACACACAA 1

RESULT 14
AZ411170/c

LOCUS

AZ411170 36 bp DNA linear GSS 03-OCT-2000

DEFINITION

IM0184D09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0184D09 F, DNA sequence.

ACCESSION

AZ411170

VERSION

AZ411170.1 GI:10535183

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 36)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0184 row: D column: 09

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 36.

Location/Qualifiers

1. .36

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0184D09"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

1 a 0 c 18 g 17 t

Query Match

0.5%; Score 27.8; DB 17; Length 36;

Best Local Similarity 93.5%; Pred. No. 4.1e+05;

Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2309 TCACACACACACACACACACACACACACA 2339

|||||

Db 35 TCACACACACACACACACACACACACACA 5

RESULT 15
AZ826021/c

LOCUS

AZ826021 37 bp DNA linear GSS 20-FEB-2001

DEFINITION

2M0101F02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0101F02 R, DNA sequence.

ACCESSION

AZ826021

VERSION

AZ826021.1 GI:12995929

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 37)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

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plasmid inserts

Unpublished (2000)

JOURNAL
COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0101 row: F column: 02

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 37.

FEATURES

Location/Qualifiers

source

1..37

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0101F02"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (g14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

0 a 0 c 18 g 19 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 0.5%; Score 27.8; DB 17; Length 37;

Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACAA 2340

Db 31 CACACACACACACACACACACACACACAA 1

RESULT 16

AZ346424/c

LOCUS

DEFINITION 1M0081N12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0081N12 R, DNA sequence.

ACCESSION AZ346424

VERSION AZ346424.1 GI:10425661

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 39)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

JOURNAL
COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0081 row: N column: 12

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 39.

FEATURES

Location/Qualifiers

source

1..39

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0081N12"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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0.005 inch orifice at constant velocity. The sheared DNA

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polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

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inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

0 a 1 c 18 g 20 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 82.1%; Score 27.8; DB 17; Length 39;

Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACAAATTATAC 2348

Db 39 CACACACACACACACACACACACACACACACACACACAA 1

RESULT 17

AZ765740/c

LOCUS

DEFINITION

AZ765740 39 bp DNA linear GSS 16-FEB-2001
1M0562C19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0562C19 R, DNA sequence.

ACCESSION AZ765740

VERSION AZ765740.1 GI:12882075

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

```

REFERENCE
AUTHORS
1 (bases 1 to 39)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0562 row: C column: 19
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 39.
FEATURES
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0562C19"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (g114732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 0 a 0 c 19 g 20 t
ORIGIN
Query Match 0.5%; Score 27.8; DB 17; Length 39;
Best Local Similarity 93.5%; Pred. No. 4e+05;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Caps 0;

QY 2310 CACACACACACACACACACACACACACAA 2340
||||| ||| ||||| ||||| |||||
Db 31 CACACACACACACACACACACACACACAA 1

RESULT 18
AZ513473/c
LOCUS
DEFINITION
AZ513473 40 bp DNA linear GSS 05-OCT-2000
clone UUGC1M0359021 R, DNA sequence.
ACCESSION
AZ513473
VERSION
AZ513473.1 GI:10694789
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 40)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0359 row: O column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 40.
FEATURES
source
1. .40
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0359021"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (g114732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 0 a 0 c 19 g 21 t
ORIGIN
Query Match 0.5%; Score 27.8; DB 17; Length 40;
Best Local Similarity 93.5%; Pred. No. 4e+05;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Caps 0;

QY 2310 CACACACACACACACACACACACACACAA 2340
||||| ||| ||||| ||||| |||||
Db 31 CACACACACACACACACACACACACACAA 1

RESULT 19
AZ606329/c
LOCUS
DEFINITION
AZ606329 32 bp DNA linear GSS 13-DEC-2000
clone UUGC1M0428K07 F, DNA sequence.
ACCESSION
AZ606329
VERSION
AZ606329.1 GI:11728519
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE 1 (bases 1 to 32)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0428 row: K column: 07
 Seq primer: CGTTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 32.
 Location/Qualifiers

FEATURES

source

1. .32
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0428K07"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 16 g 16 t
 ORIGIN

Query Match 0.5%; Score 27.2; DB 17; Length 32;
 Best Local Similarity 90.6%; Pred. No. 5.5e+05;
 Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2311 ACACACACACACACACACACACACACACAC 2342
 Db 32 ACACACACACACACACACACACACACACCA 1

RESULT 20
 AZ834388/c
 LOCUS 33 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0117N01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0117N01 F, DNA sequence.
 ACCESSION AZ834388
 VERSION 1 GI:13004296
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 33)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0117 row: N column: 01
 Seq primer: CGTTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 33.
 Location/Qualifiers

FEATURES

source

1. .33
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0117N01"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 0 c 17 g 15 t
 ORIGIN

Query Match 0.5%; Score 27.2; DB 17; Length 33;
 Best Local Similarity 90.6%; Pred. No. 5.5e+05;
 Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACAC 2341
 Db 33 CACACACACACACACACACACACACACACC 2

RESULT 21
 AZ373001/c
 LOCUS 36 bp DNA linear GSS 02-OCT-2000
 DEFINITION 1M0125A12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0125A12 F, DNA sequence.
 ACCESSION AZ373001
 VERSION 1 GI:10486701
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 37)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0215 row: L column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 37.

FEATURES

source

Location/Qualifiers

1..37

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0215L08"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

3 a 0 c 17 g 17 t

Query Match 0.5%; Score 27; DB 17; Length 37;
Best Local Similarity 85.7%; Pred. No. 6e+05;
Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACAT 2344

||||||| ||| ||||||||| ||| |||
Db 35 CACACACACACACACACACACACACACTTAT 1

RESULT 28

AZ305049/c

LOCUS

DEFINITION AZ305049 40 bp DNA linear GSS 29-SEP-2000
clone UUGC1M0005B05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DNA sequence.

ACCESSION AZ305049

VERSION AZ305049.1 GI:10341678

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

1 (bases 1 to 40)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0005 row: B column: 05
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 40.

Location/Qualifiers

1..40

/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="UUGC1M0005B05"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

1 a 0 c 19 g 20 t

Query Match 0.5%; Score 27; DB 17; Length 40;
Best Local Similarity 85.7%; Pred. No. 5.9e+05;
Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACAT 2344

||||||| ||| ||||||||| ||| |||
Db 35 CACACACACACACACACACACACACACAT 1

RESULT 29

AZ475919/c

LOCUS

DEFINITION AZ475919 30 bp DNA linear GSS 04-OCT-2000
clone UUGC1M0294P15 F, DNA sequence.

ACCESSION AZ475919

VERSION AZ475919.1 GI:10634044

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;

[illegible]

REFERENCE
AUTHORS

1 (bases 1 to 32)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0246 row: M column: 11

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 32.

FEATURES
source

Location/Qualifiers

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/organism="Mus musculus"

/strain="C57BL/6J"

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/clone="UUGC1M0246M11"

/clone.lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

0 a 0 c 15 g 17 t

Query Match

Best Local Similarity 0.5%; Score 26.8; DB 17; Length 32;

Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2311

ACACACACACACACACACACACACAA 2340

||||||| ||| ||||| ||||| |||||

Db 32

ACACACACACACACACACACACACAA 3

RESULT 44

AZ495235/c

LOCUS

DEFINITION

IM0331E05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0331E05 F, DNA sequence.

ACCESSION

AZ495235

VERSION

AZ495235.1 GI:10670567

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 32)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0331 row: E column: 05

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 32.

FEATURES
source

Location/Qualifiers

1..32

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0331E05"

/clone.lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

0 a 0 c 16 g 16 t

Query Match

Best Local Similarity 0.5%; Score 26.8; DB 17; Length 32;

Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2310

CACACACACACACACACACACACACA 2339

||||||| ||| ||||| ||||| |||||

Db 32

CACACACACACACACACACACACACA 3

RESULT 45

AZ464370/c

LOCUS

DEFINITION

IM0273P11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0273P11 R, DNA sequence.

ACCESSION

AZ464370

VERSION

AZ464370.1 GI:10622495

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

